

FIG. 1A

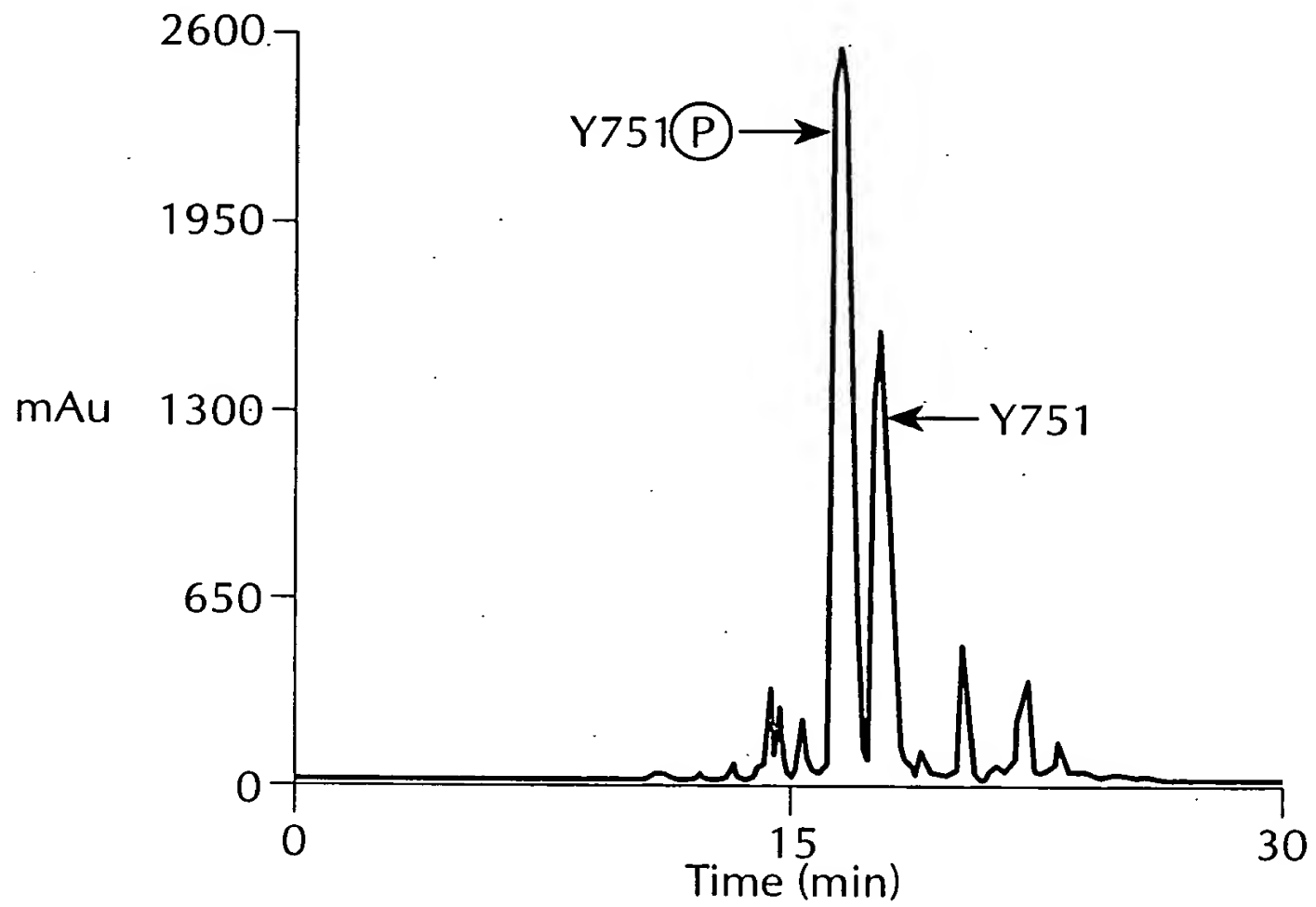


FIG. 1B

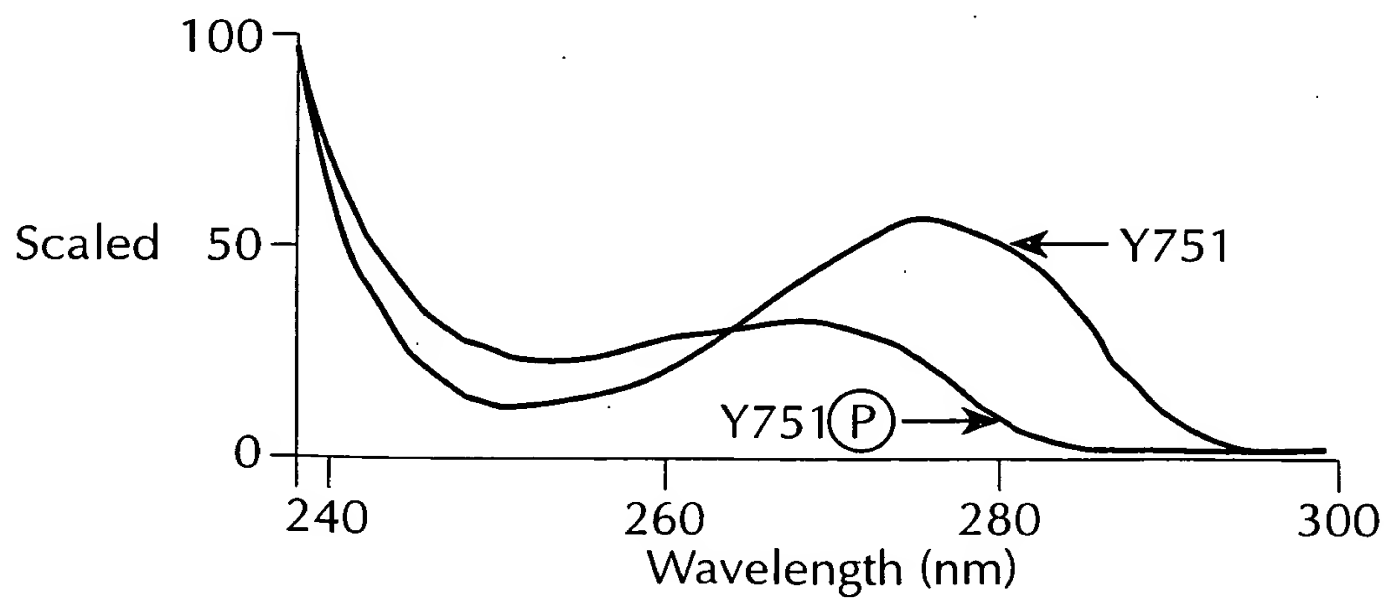


FIG. 1C

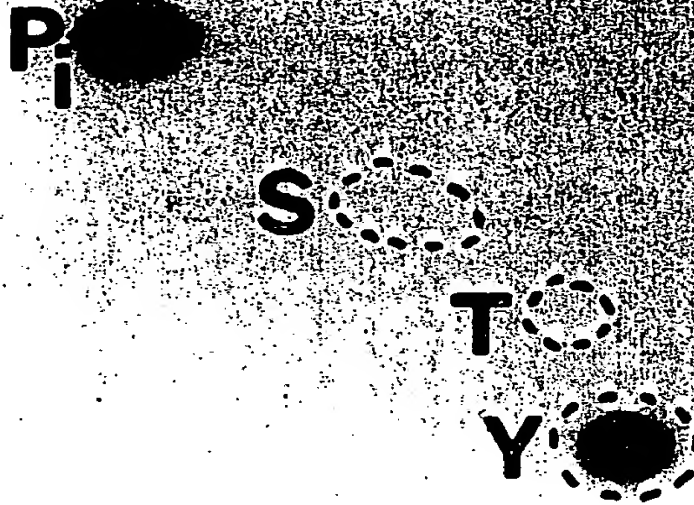


FIG. 1D

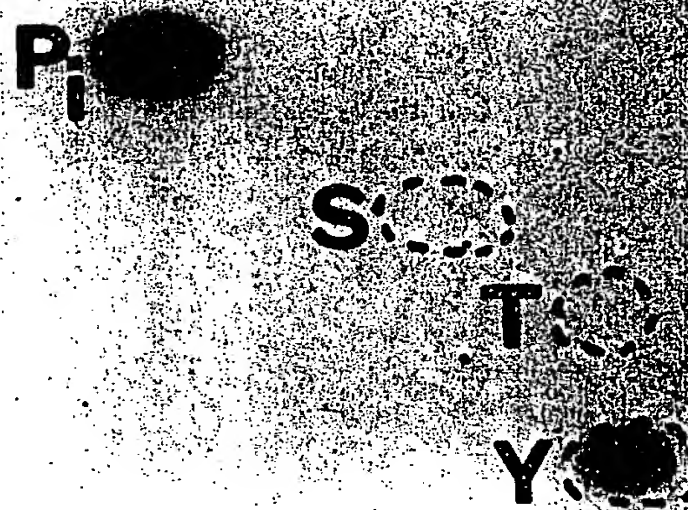


FIG. 2A

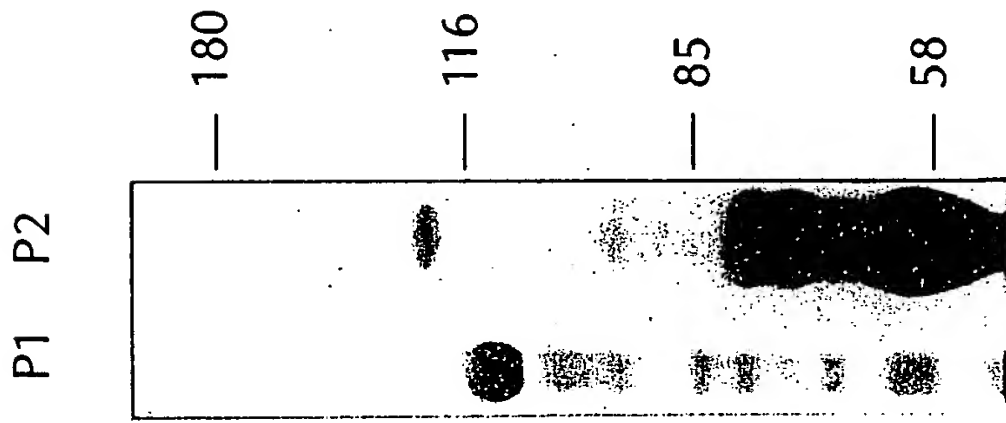
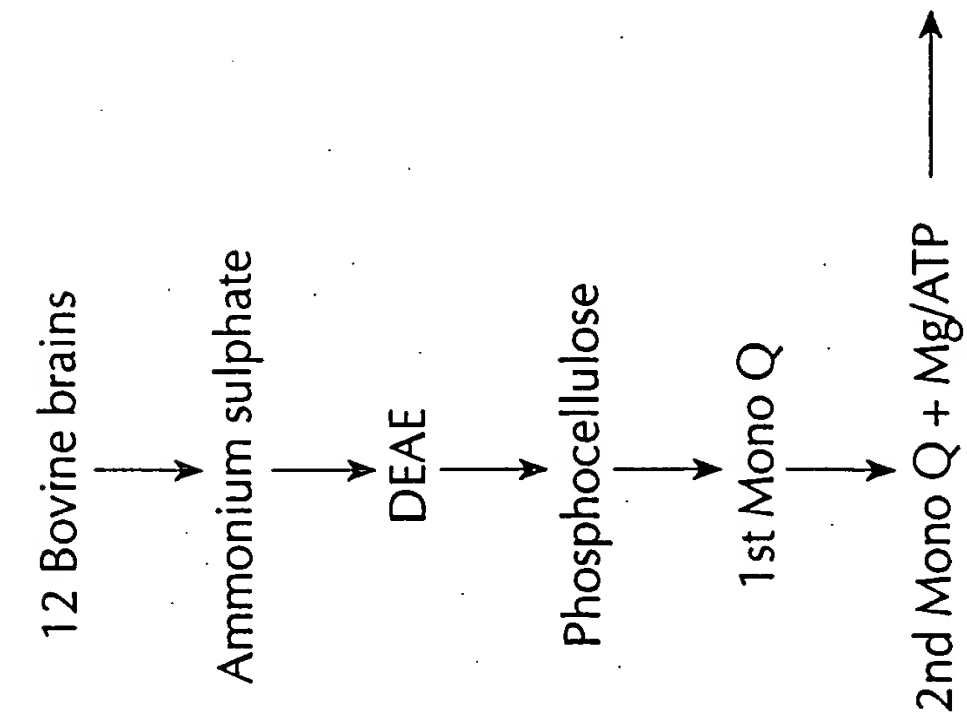


FIG. 2B

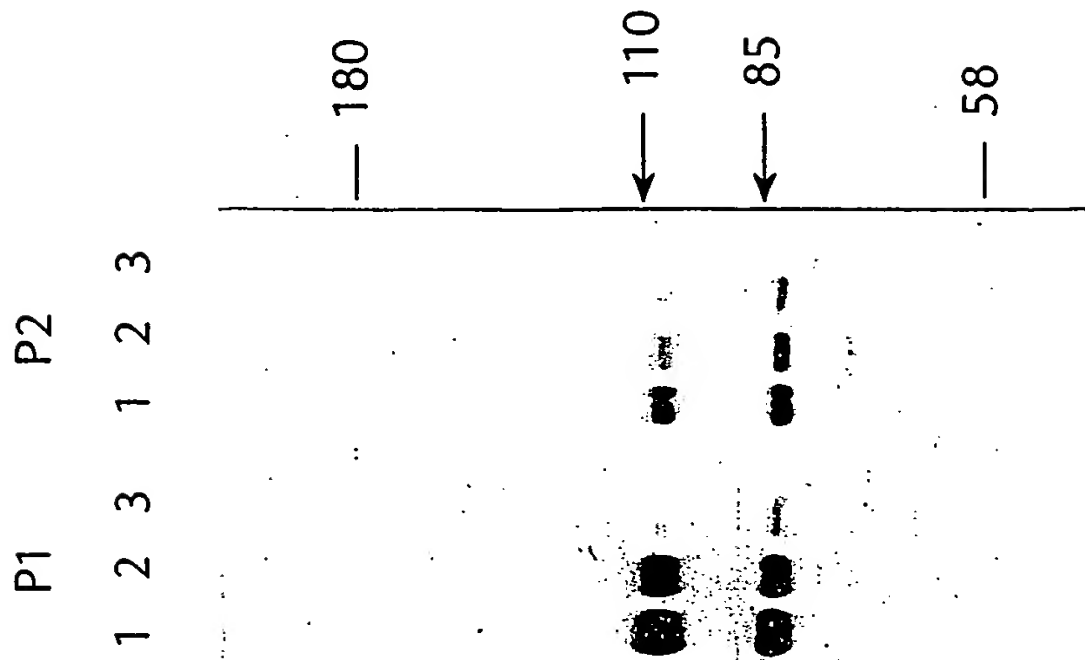


FIG. 3

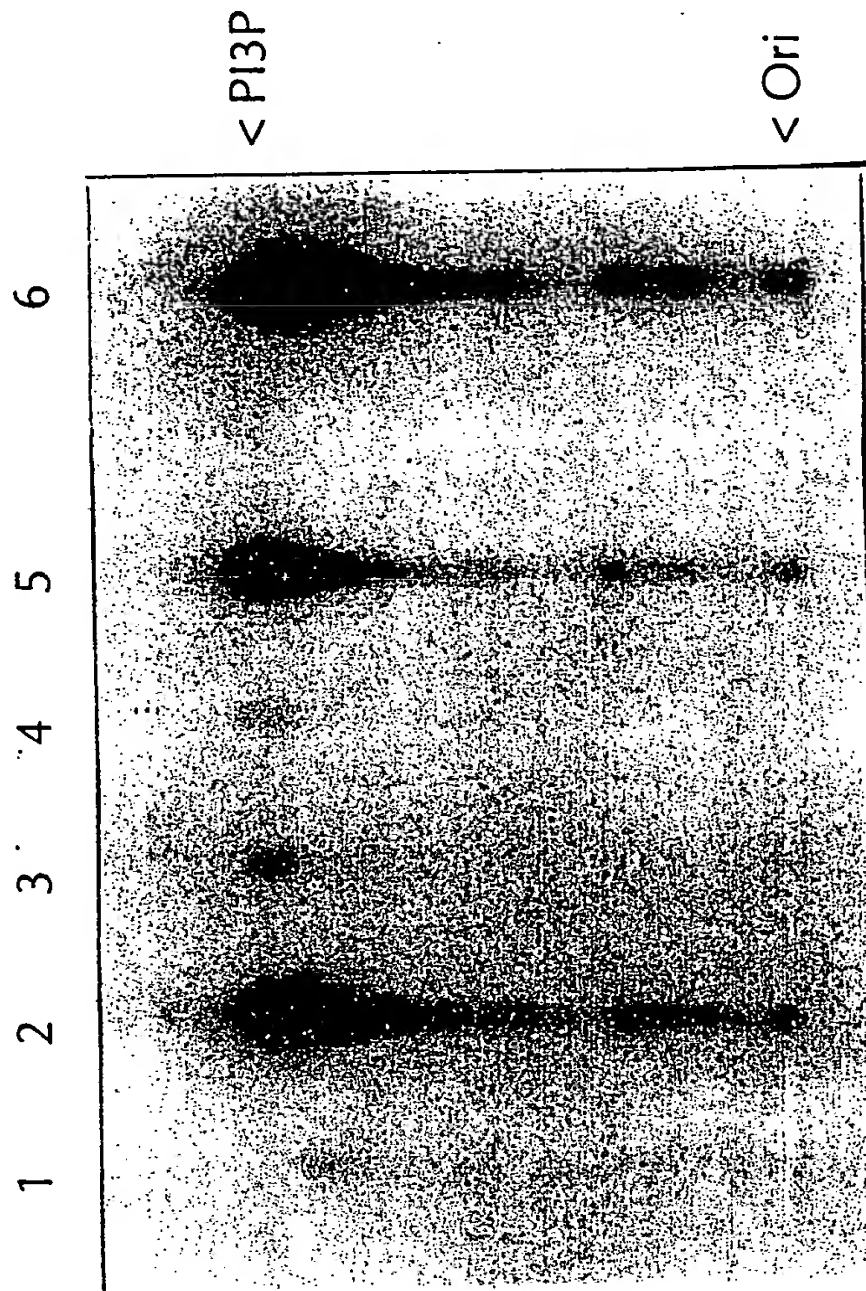


FIG. 4B



FIG. 4C

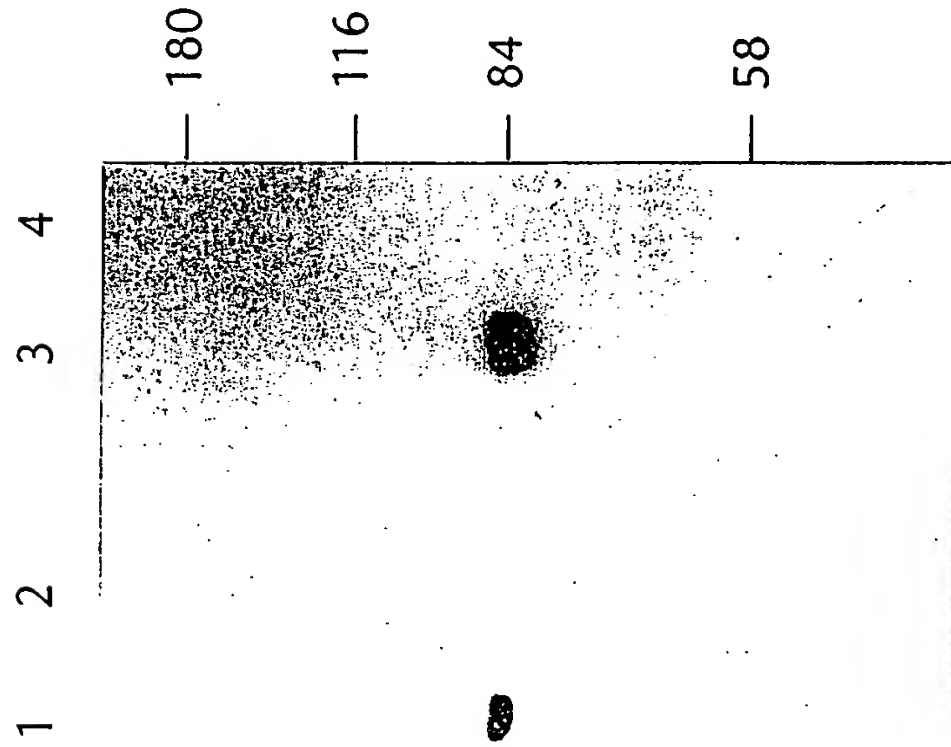


FIG. 4D

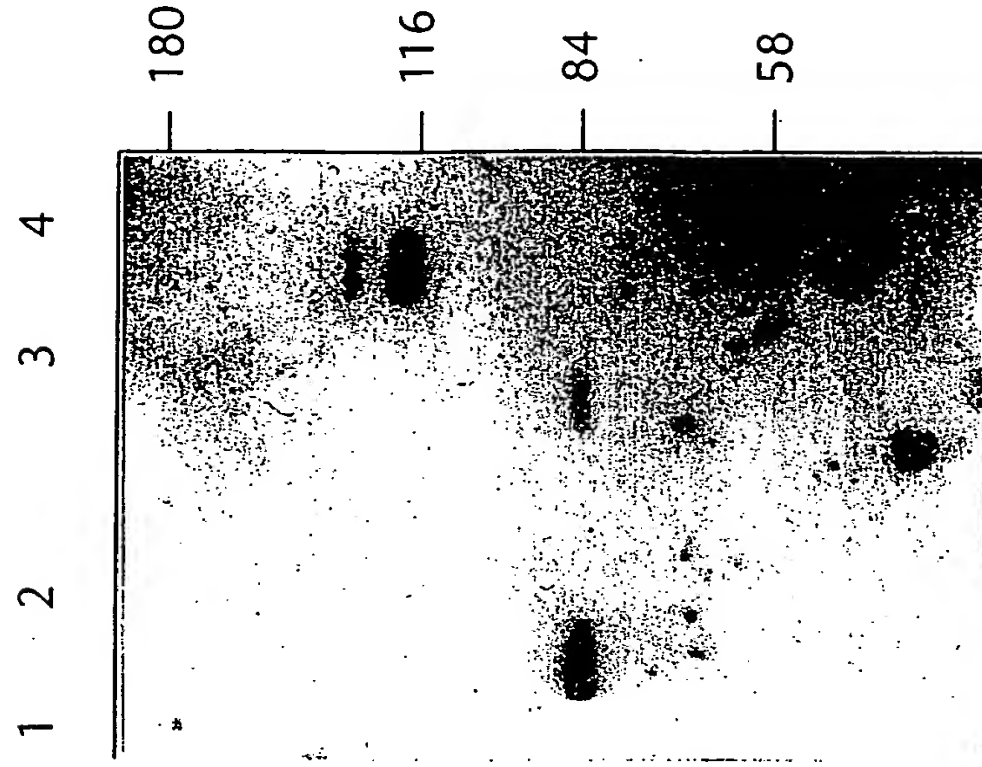


FIG. 5A

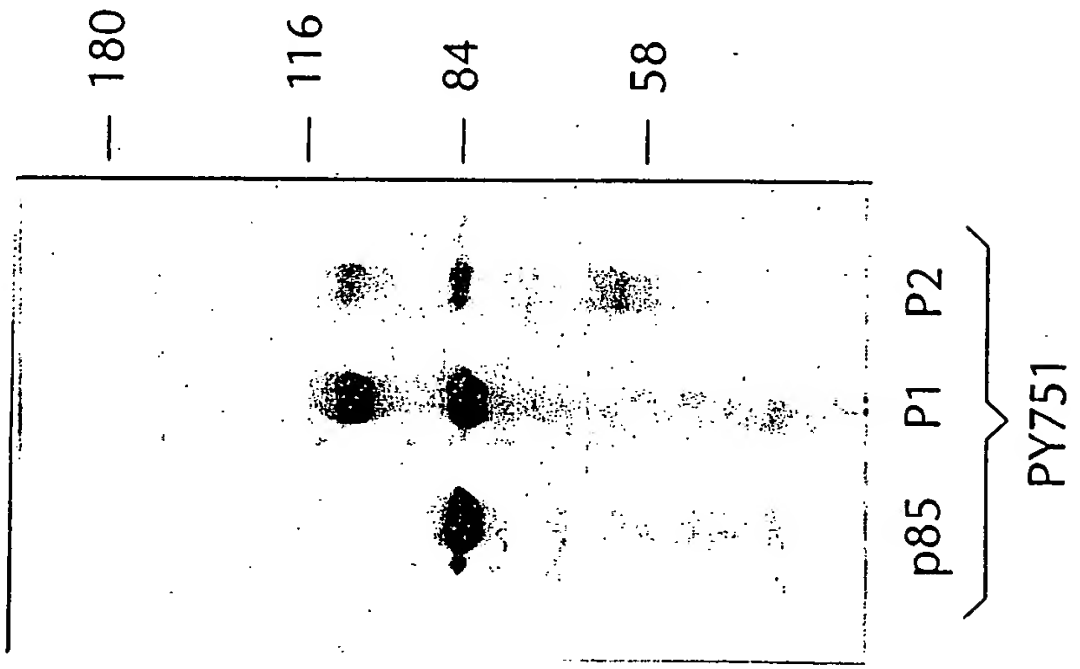


FIG. 5B

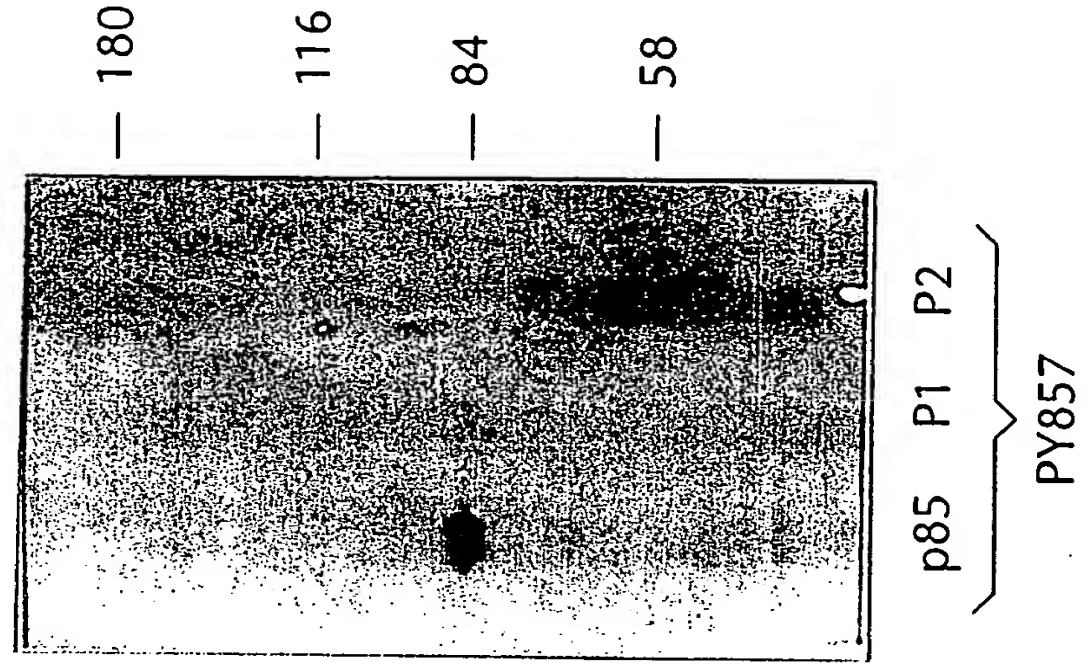


FIG. 6A

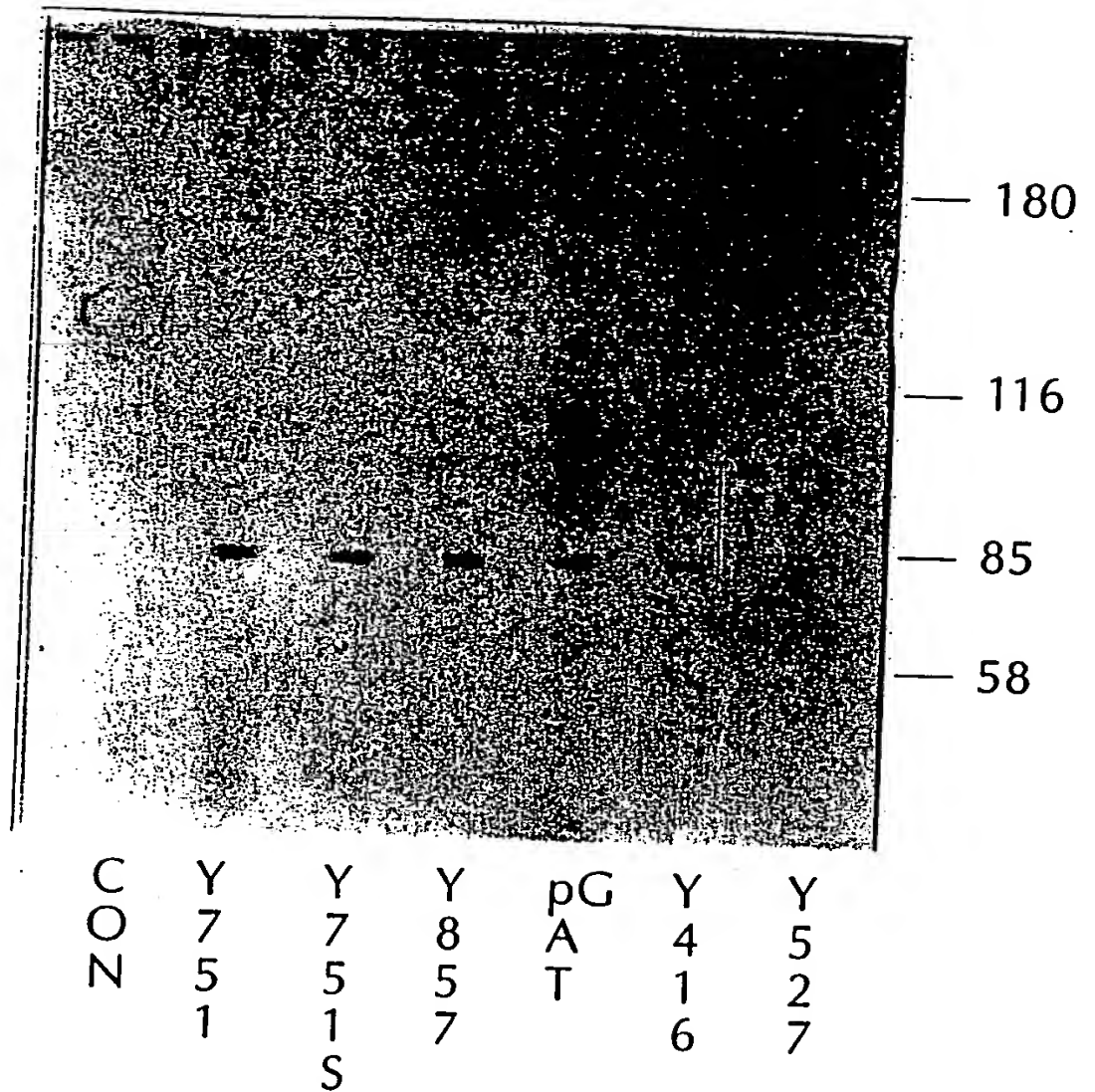


FIG. 6B

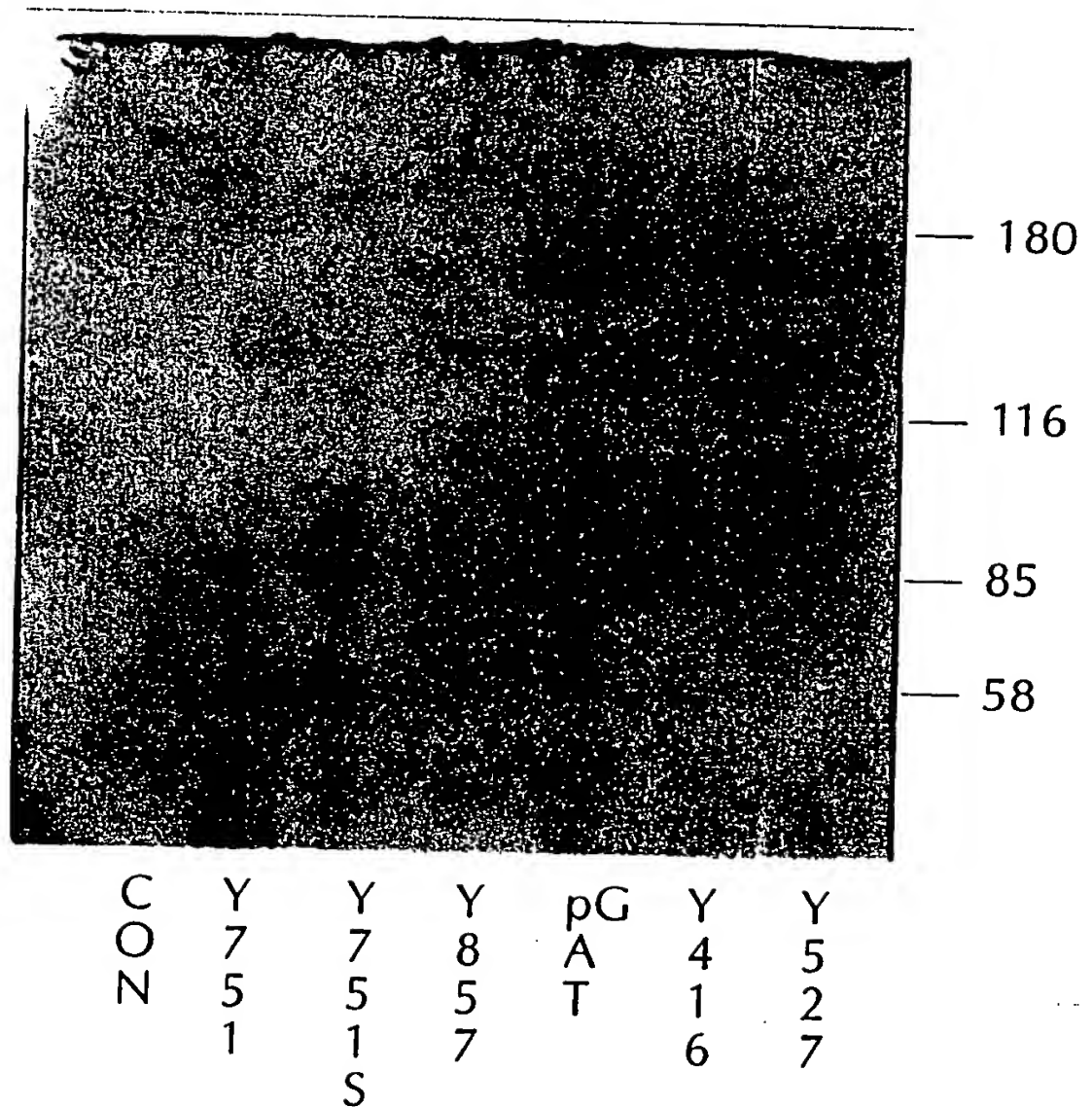


FIG. 7A

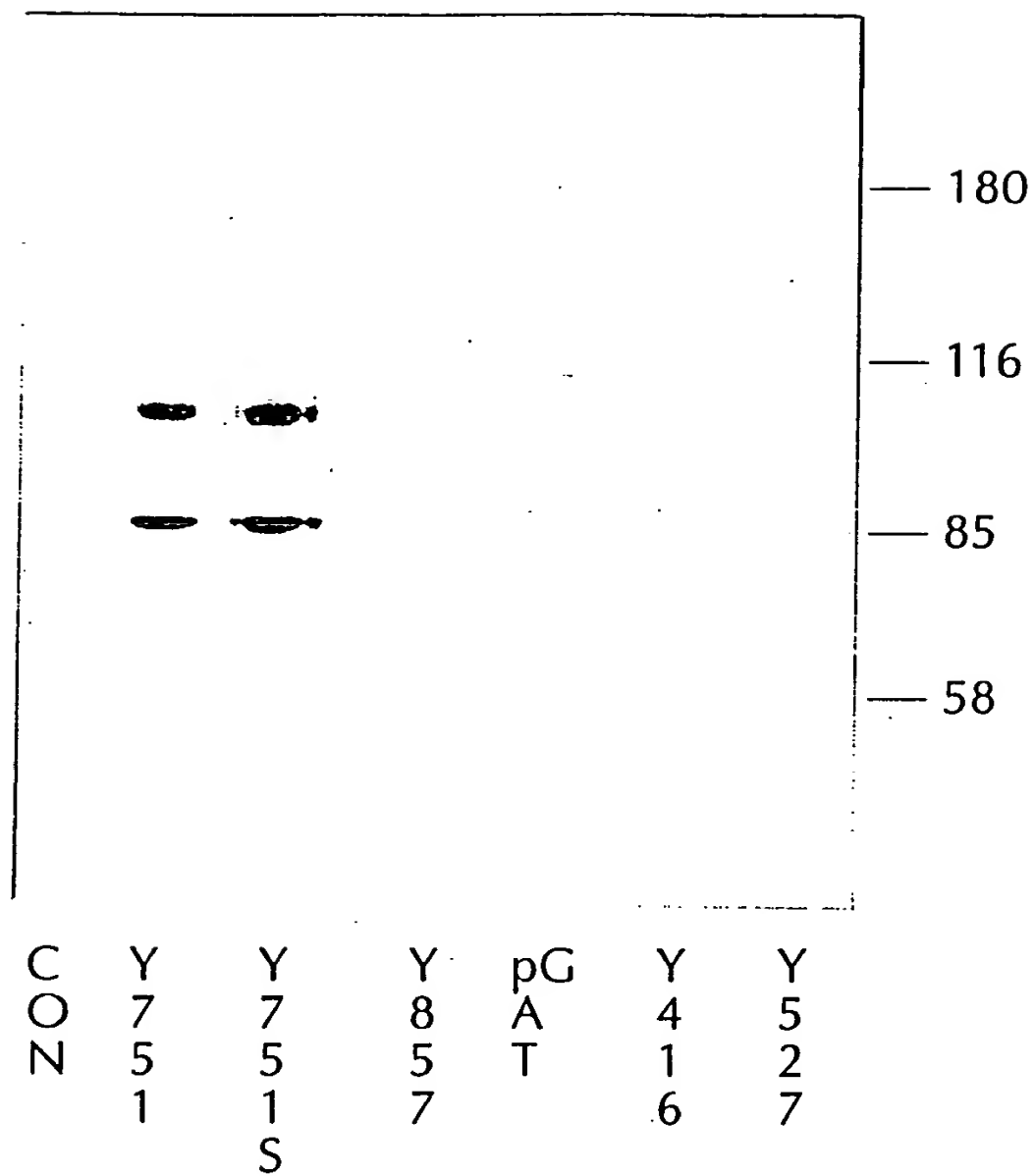


FIG. 7B

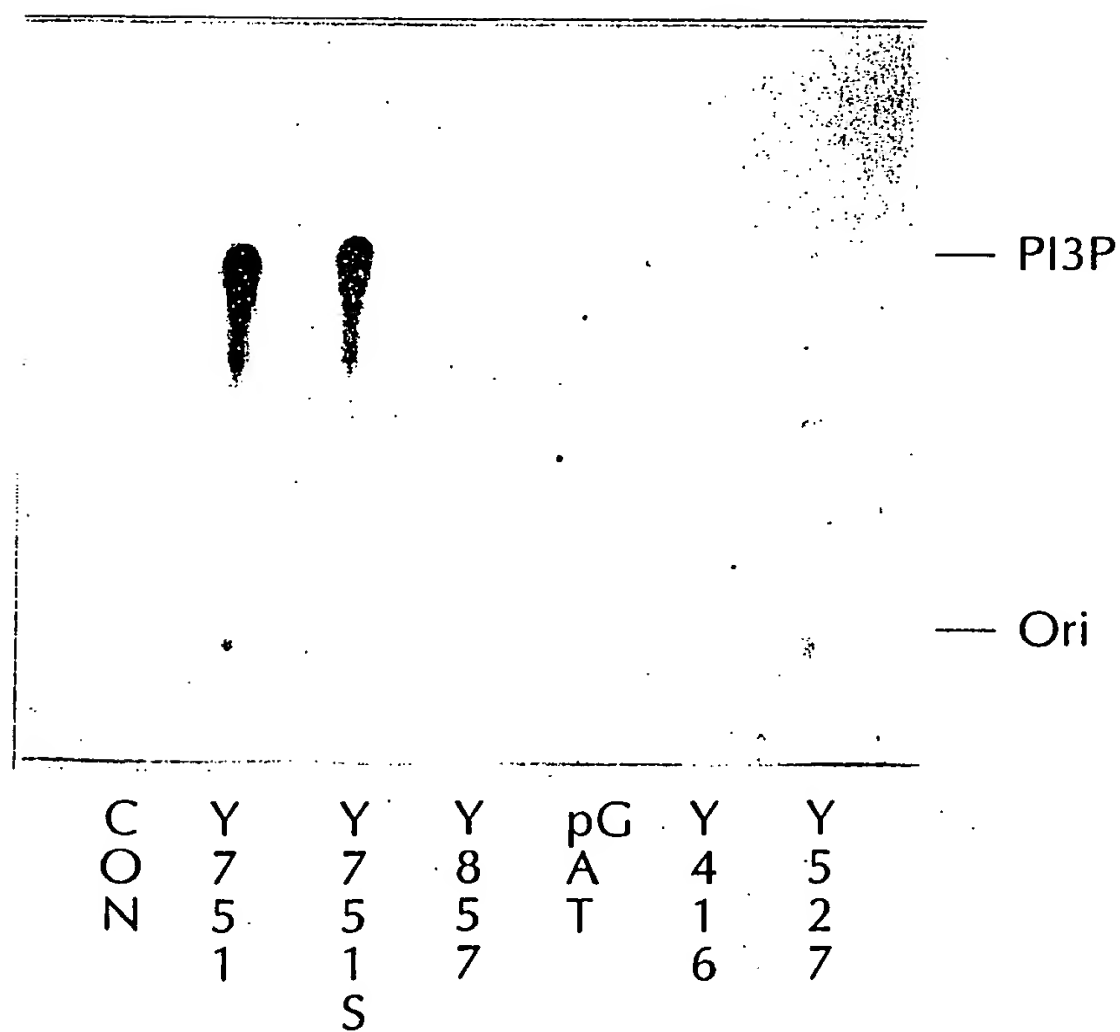


FIG. 8A

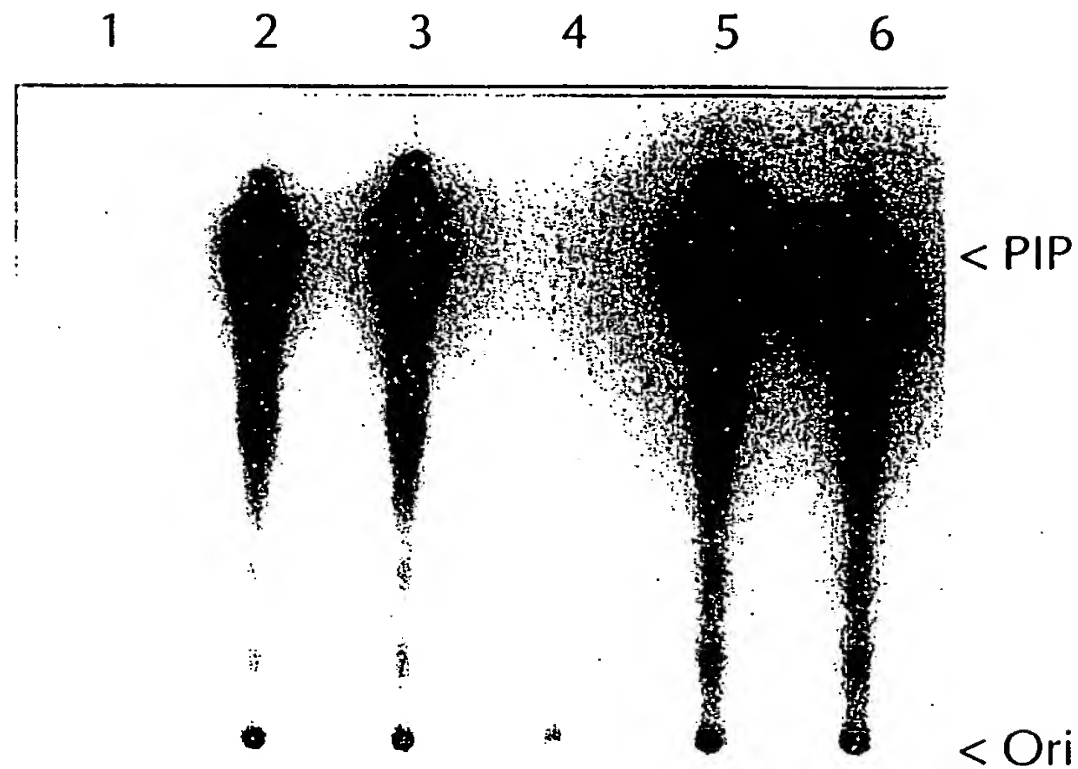


FIG. 8B

| | |
|-----------|-----------------------------------|
| 751 | D M S K D E S V D Y V P M L D M K |
| 751.S | C D E S V D Y V P M L |
| 740 | G E S D G G Y M D M S K |
| 1313 | E F C P D P L Y E V M L K |
| Consensus | E E E E E Y M P M X X |
| | D D D D D V |

FIG. 9A

| | |
|---|-----|
| M P P R P S S G E L W G I H L M | 16 |
| ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG | 48 |
| P P R I L V E C L L P N G M I V | 32 |
| CCCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGGATGATAGTG | 96 |
| T L E C L R E A T L I T I K H E | 48 |
| ACTTTAGAATGCCTCCGTGAGGCTACGTTAATAACGATAAAGCATGAA | 144 |
| L F K E A R K Y P L H Q L L Q D | 64 |
| CTATTTAAAGAAGCAAGAAAATACCCTCTCCATCAACTTCTTCAAGAT | 192 |
| E S S Y I F V S V T Q E A E R E | 80 |
| GAATCTTCTTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA | 240 |
| E F F D E T R R L C D L R L F Q | 96 |
| GAATTTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAA | 288 |
| P F L K V I E P V G N R E E K I | 112 |
| CCCTTTTTTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATC | 336 |
| L N R E I G F A I G M P V C E F | 128 |
| CTCAATCGAGAAATTGGTTTTTGCTATCGGCATGCCAGTGTGTGAATTC | 384 |
| D M V K D P E V Q D F R R N I L | 144 |
| GATATGGTTAAAGATCCAGAAGTACAGGACTTCCGAAGAAATATTCTC | 432 |

FIG. 9B

N V C K E A V D L R D L N S P H 160
AATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT 480
A
S R A M Y V Y P P N V E S S P E 176
AGTAGAGCAATGTATGTTTATCCTCCAAATGTAGAATCTTCACCAGAA 528
L P K H I Y N K L D K G Q I I V 192
CTGCCAAAGCACATATATAATAAATTGGATAAAGGGCAAATAATAGTG 576
V I W V I V S P N N D K Q K Y T 208
GTGATTGGGTAATAGTTTCTCCAAATAATGACAAACAGAAGTATACT 624
L K I N H D C V P E Q V I A E A 224
CTGAAAATCAACCATGACTGTGTGCCAGAACAAGTAATTGCTGAAGCA 672
I R K K T R S M L L S S E Q L K 240
ATCAGGAAAAAACTCGAAGTATGTTGCTATCATCTGAACAACTAAAA 720
L C V L E Y Q G K Y I L K V C G 256
CTCTGTGTTT TAGAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA 768
C D E Y F L E K Y P L S Q Y K Y 272
TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTAT 816
I R S C I M L G R M P N L M L M 288
ATAAGAAGCTGTATAATGCTTGGGAGGATGCCCAATTTGATGCTGATG 864

FIG. 9C

A K E S L Y S Q L P M D C F T M 304
GCTAAAGAAAGCCTCTATTTCTCAACTGCCAATGGACTGTTTTACAATG 912

P S Y S R R I S T A T P Y M N G 320
CCATCATATTCCAGACGCATCTCCACAGCTACGCCATATATGAATGGA 960

^B
E T S T K S L W V I N S A L R I 336
GAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCCTCAGAATA 1008

K I L C A T Y V N V N I R D I D 352
AAAATTCTTTGTGCAACCTATGTGAATGTAAATATTCGAGACATTGAC 1056

K I Y V R T G I Y H G G E P L C 368
AAGATTTATGTTGGAACAGGTATCTACCATGGAGGAGAACCCTTATGT 1104

D N V N T Q R V P C S N P R W N 384
GATAATGTGAACACTCAAAGAGTACCTTGTTCCTCAATCCCAGGTGGAAT 1152

E W L N Y D I Y I P D L P R A A 400
GAATGGCTGAATTACGATATATACATTCCTGATCTTCCTCGTGCTGCT 1200

R L C L S I C S V K G R K G A K 416
CGACTTTGCCTTTCCATTTGTTCTGTAAAGGCCGAAAGGGTGCTAAA 1248

E E H C P L A W G N I N L F D Y 432
GAGGAACACTGTCCATTGGCCTGGGGAAATATAAACTTGTTTGATTAC 1296

FIG. 9D

| | |
|--|------|
| T D T L V S G K <u>M A L N L W P V</u> | 448 |
| ACAGATACTCTAGTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTA | 1344 |
| <u>P H G L E D L L N P I G V T G S</u> | 464 |
| CCTCATGGACTAGAAGATTGCTGAACCCTATTGGTGTTACTGGATCA | 1392 |
| N P N K E T P C L E L E F D W F | 480 |
| AATCCAAATAAAGAACTCCATGTTTAGAGTTGGAGTTTGACTGGTTC | 1440 |
| S S V V K F P D M S V I E E H A | 496 |
| AGCAGTGTGGTAAAGTTTCCAGATATGTCAGTGATTGAAGAGCATGCC | 1488 |
| N W S V S R E A G F S Y S H A G | 512 |
| AATTGGTCTGTATCCCGTGAAGCAGGATTTAGTTATTCCCATGCAGGA | 1536 |
| L S N R L A R D N E L R E N D K | 528 |
| CTGAGTAACAGACTAGCTAGAGACAATGAATTAAGAGAAAATGATAAA | 1584 |
| E Q L R A I C T R D P L S E I T | 544 |
| GAACAGCTCCGAGCAATTTGTACACGAGATCCTCTATCTGAAATCACT | 1632 |
| E Q E K D F L W S H R H Y C V T | 560 |
| GAGCAAGAGAAAGATTTTCTGTGGAGCCACAGACACTATTGTGTAAC | 1680 |
| I P E I L P K L L L S V K W N S | 576 |
| ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAAC | 1728 |

FIG. 9E

R D E V A Q M Y C L V K D W P P 592
AGAGATGAAGTAGCTCAGATGTACTGCTTGGTAAAAGATTGGCCTCCA 1776

I K P E Q A M E L L D C N Y P D 608
ATCAAGCCTGAACAGGCTATGGAGCTTCTGGACTGCAATTACCCAGAT 1824

P M V R G F A V R C L E K Y L T 624
CCTATGGTTCGAGGTTTTGCTGTTTCGGTGCTTAGAAAAATATTTAACA 1872

D
D D K L S O Y L I O L V O V L K 640
GATGACAAACTTTCTCAGTACCTAATTCAGCTAGTACAGGTACTAAAA 1920

Y E O Y L D N L L V R F L L K K 656
TATGAACAGTATTTGGATAACCTGCTTGTGAGATTTTACTCAAAAAA 1968

E
A L T N O R I G H F F F W H L K 672
GCGTTAACTAATCAAAGGATCGGTCACTTTTCTTTTGGCATTTAAAA 2016

F
S E M H N K T V S O R F G L L L 688
TCTGAGATGCACAATAAAACAGTTAGTCAGAGGTTTGGCCTGCTTTTG 2064

E S Y C R A C G M Y L K H L N R 704
GAGTCCTATTGCCGTGCATGTGGGATGTATCTGAAGCACCTTAATAGG 2112

G
Q V E A M E K L I N L T D I L K 720
CAAGTTGAGGCTATGGAAAAGCTCATTAACTTGACTGACATTCTCAA 2160

FIG. 9F

| | |
|---|------|
| Q E K K D E T Q K V Q M K F L V | 736 |
| CAAGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT | 2208 |
| E Q M R R P D F M D A L Q G F L | 752 |
| GAGCAAATGCGGCGACCAGATTTTCATGGATGCTCTCCAGGGCTTTCTG | 2256 |
| S P L N P A H Q L G N L R L E E | 768 |
| TCTCCTCTAAACCTGCTCATCAGCTGGGAAATCTCAGGCTTGAAGAG | 2304 |
| C R I M S S A K R P L W L N W E | 784 |
| TGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGGAG | 2352 |
| N P D I M S E L L F Q N N E I I | 800 |
| AACCCAGACATCATGTGAGAATTACTCTTTCAGAACAAATGAGATCATC | 2400 |
| F K N G D D L R Q D M L T L Q I | 816 |
| TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACCCTTCAGATT | 2448 |
| I R I M E N I W Q N Q G L D L R | 832 |
| ATTCGCATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGA | 2496 |
| M L P Y G C L S I G D C V G L I | 848 |
| ATGTTACCTTATGGATGTCTGTCAATCGGTGACTGTGTGGGACTTATC | 2544 |
| E V V R N S H T I M Q I Q C K G | 864 |
| GAGGTGGTGAGAAATTCTCACACTATAATGCAGATTCAGTGTAAGGA | 2592 |

FIG. 9G

G L K G A L O F N S H T L H O W 880
GGCCTGAAAGGTGCACTGCAGTTTAACAGCCACACACTCCATCAGTGG 2640

L K D K N K G E I Y D A A I D L 896
CTCAAAGACAAGAACAAGGGGGGAAATATATGATGCGGCCATCGATTG 2688

F T R S C A G Y C V A T F I L G 912
TTTACACGATCATGTGCTGGATATTGTGTTGCCACCTTCATTTTGGGA 2736

I G D R H N S N I M V K D D G O 928
ATTGGAGATCGTCACAATAGTAATATCATGGTTAAAGATGATGGACAA 2784

L F H I D F G H F L D H K K K K 944
CTGTTTCATATAGATTTTGGACACTTTTGGGATCACAAGAAGAAAAA 2832

F G Y K R E R V P F V L T O D F 960
TTTGGTTATAAACGAGAGCGCGTGCCGTTTGTTTTGACACAAGATTTC 2880

L I V I S K G A Q E C T K T R E 976
TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAGAA 2928

F E R F Q E M C Y K A Y L A I R 992
TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGG 2976

FIG. 9H

Q H A N L F I N L F S M M L G S 1008
CAGCATGCCAATCTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCT 3024

G M P E L Q S F D D I A Y I R K 1024
GGAATGCCAGAACTGCAATCTTTTGATGATATTGCATACATTGAAAG 3072

T L A L D K T E O E A L E Y F M 1040
ACCCTAGCTTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTTCATG 3120

K Q M N D A H H G G W T T K M D 1056
AAACAAATGAATGATGCACACCATGGTGGCTGGACAACAAAATGGAT 3168

W I F H T I K Q H A L N * 1069
TGGATCTTCCACACAATTAAGCAGCATGCTTTGAACTGA 3207

FIG. 9I

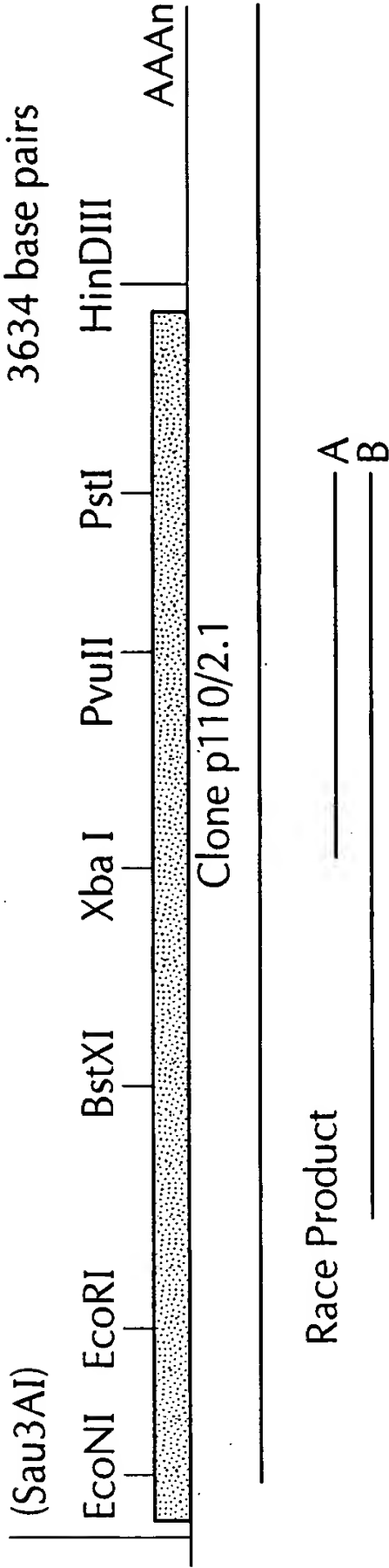


FIG. 10A

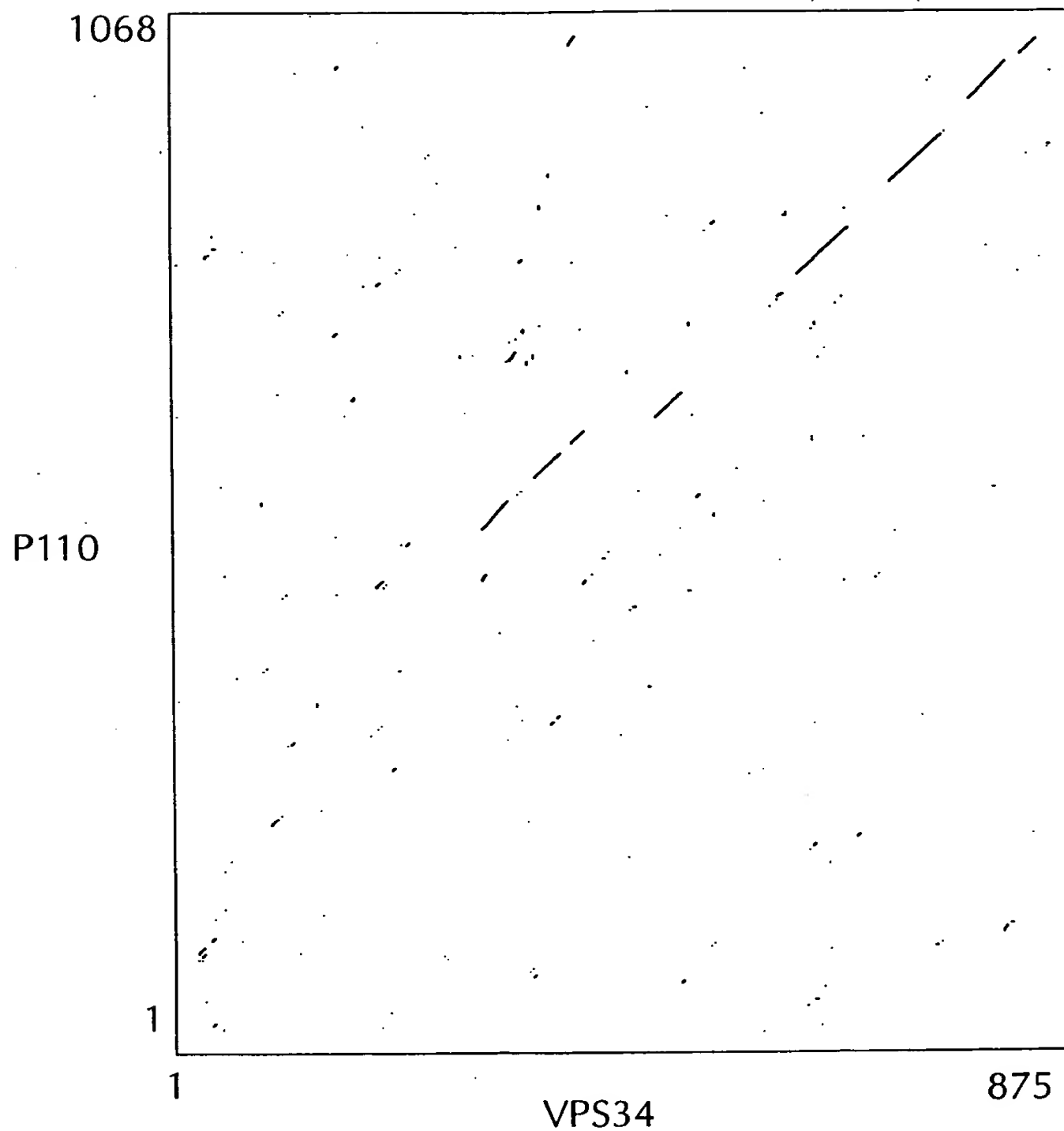


FIG. 10B

P110 VCEEDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHSRAMYVYPPN 170
..| : .| :|. :: .| .: . : |:. :...|
VPS34 NITFCVSLQDLDP.LKVKIKSLEGHKPLLKPSQKILNPELMLIGSN 49
171 VESSPEL..PKHIYNKLDKGQIIVVIWVTVSPNNDKQKYTLKINHDCVPE 218
|.|.:.| . :::| . :...|:. | :...:..
50 VFPSSDLIVSLQVFDKERNRNLTLPIYTPYIPFRNSRTWDYWL..... 92
219 QVIAEAIRKKTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLS 268
.. ::: : :|| :|:::|..|
93TLPIRIKQLTFSS.HLRIILWEYNG..... 116
269 QYKYIRSCIMLGRMPNMLMAKESLYSQLPMDCFMPYSRRISTATPYM 318
|...|:
117SKQIPFF 123
319 NGETSTKSLWVINSALRIKILCATYVNVNIRDIDKIYVRTGIYHGGEPLC 368
| |||. : : :..|: |::: .| :... .|..
124 NLETSI..FNLKDCTLK.....RGFESLKFRYDVIDHCEVVT 158
369 DNVNTQRVPCSNPRWNEWLNYDIYIPDLPRARLC.LSICSVKGRKGAKE 417
|| : .| || ..: :..| :| :. :::: :...:
159 DNKD.....QENLN.KYFQGEFTRLPLWLDEITISKLRKQRENRT 196

FIG. 10C

418 .EHCPLAWG.NINLFDYTDTLVSGKMAINLWPVPHGLEDLLNPIGVTGS. 464
..... :: :: : | . | | | :....
197 WPQGTFVLNLEFPMLELPVVFIEREIMNTQMNIP....TLKNNPGLSTDL 242
465 .NPNKETPCLELEF.DWFSSVVKFPDMSVIEEHANWSVSREAGFSYSHAG 512
: || : : . | : : : : | . : | . : || | : : : | . . | : : : | :
243 REPNRNDPQIKISLGDKYHSTLKFYD....PDQPNNDPIEEKYRRLERAS 288
513 LSNRLARDNELRENDKEQLRAICTRDPLSEITEQEKDFLWSHRHYCVTIP 562
... | : : . . : : | . | . . | : : | : : || : : | . . | . | : . .
289 KNANLDKQVKPDIKKRDYLNKIINYP PGTKLTAHEKGSIWKYRYIIMNNK 338
563 EILPKLLLSVKWNSRDEVAQMYCLVKDWPP IKPEQAMELLDCNYPDPMVR 612
 . | . || | | | . : : . . . | : : . | : . . | : . . : : | : || : : : : : ||
339 KALTKLLQSTNLREESERVEVLELMDSWAEIDIDDALELLGSTFKNLSVR 388
613 GFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQY..... 644
 : : || . | . | . | . . | : || : || : : : : | . .
389 SYAVNRLKK.ASDKELELYLLQLVEAVCFENLSTFSDKSNSEFTIVDAVS 437
645LDNLLVRELLKK 656
 : . | . || : : :
438 SQKLSGDSMLLSTSHANQKLLKSISSESETSGTESLP IVISPLAEFLIRR 487

FIG. 10D

657 ALTNQRIGHFFFWHLKSEMHNKTVSQRFGLLESY.CRACGMYLKHLNRQ 705
||.|.|:| ||:|.|||| .:|. .: .:|.|: :| . . |||
488 ALVNPRLGSFFYWYLKSESEDKPY...LDQILSSFW SRLDKKSRN ILNDQ 534
706 VEAMEKLINLTDILKQEKKDETQKVQMKF.LVEQMRRPDEM DALQGF LSP 754
| : : | : . . . :|. |. . . . | : : : . | : | . || : : . . : |
535 VRLINVLRECCETIKRLKDTTAKKMELLVHLL ETKV RP..LVKVRPIALP 582
755 LNPAHQ LGNLRLEECRIMSSAKRPLWLNWENPDIMSELLFQNN E IIFKNG 804
| : |. . : : |. : : : :|. . ||. : : | | . : : || |
583 LDPDV LICDVCPETSKVFKSSLSPLKITFKTT.....LNQPYHLMFKVG 626
*
805 DDLRQDMLTLQIIRIMENIWQNOGLDLRMLPYGCLSIGDCVGLIEVVRNS 854
||||| |. : |||. : | : : : :|. : : : ||. |. . |. | ||. : . |
627 DDLRQDQLVVQIISLMNELLKNENVDLKLTPYKILATGPQEGAT E FIPN. 675
*
855 HTIMQIQCK.GGLKGALQFNSHTLHQWLKDKNKGEIYDAAIDLETRSCAG 903
. | : | : | | : | |. : : : : : | |. : | |||
676 DTLASILSKYHGILGYLKL.....HYPDENATLG VQGWLDNFVKSCAG 719
* * ***
904 YCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVP 953
||| | : ||| : ||| |. | : : |. . | : : || | ||| : | : : . . |. |
720 YCVITYILGVGDRHLDNLLVTPDGHFFHADFGYILGQDPKPF.....P 762
954 FVLTQDFLIVISKGAQECTKTREFFERFQEMCYKAYLAIRQHANLFINLFS 1003
: . . | : . | : | : . : : : |. . | : || : |. : |. | : : |||. |
763 PLMKLPPQIIEAFGGAESS...NYDKFRSYCFVAYSILRRNAGLILNLFE 809
1004 MMLGSGMPE..LQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGW 1051
: | . |. : | : : . . : | : |. : . | : . . | : : | . | . : ||. : : :
810 LMKTSNIPDIRIDPNGAILRVRRERFNLNMSEEDATVHFQNLINDSVNALL 859
1052 TTKMDWIFHTIKQH 1065
.. : | : |. : |.
860 PIVIDH.LHNLAQY 872

FIG. 11B

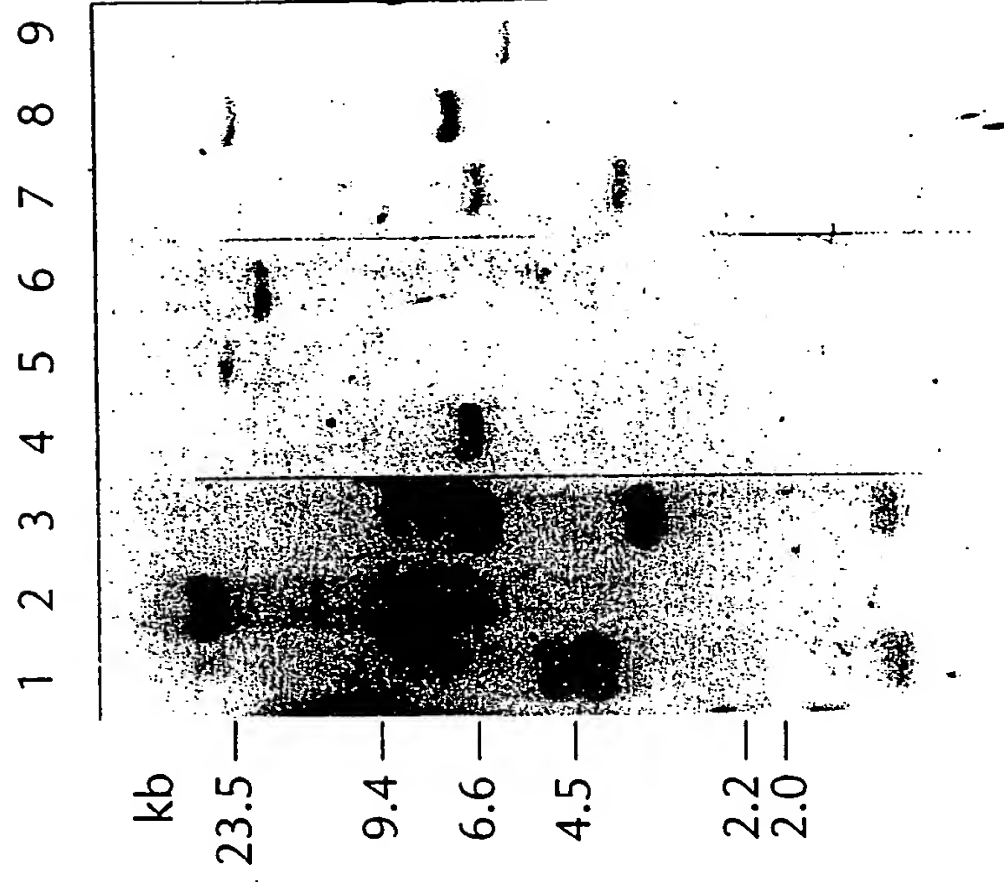


FIG. 11A

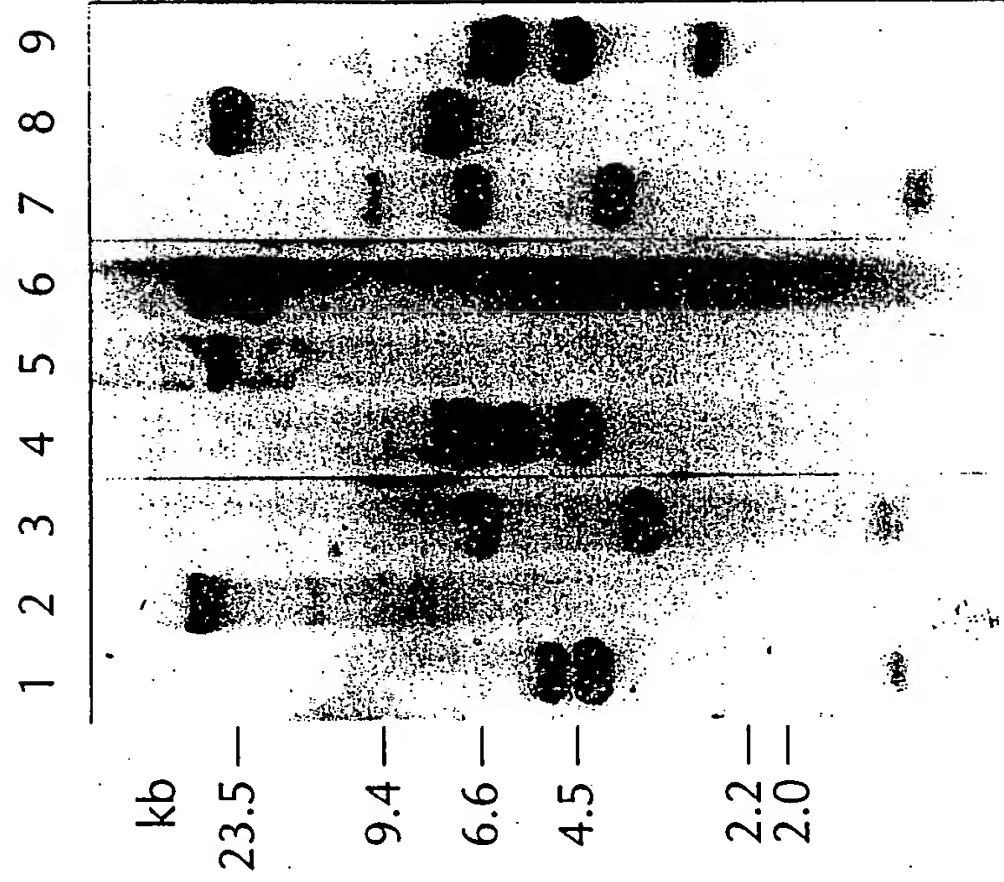


FIG. 12A

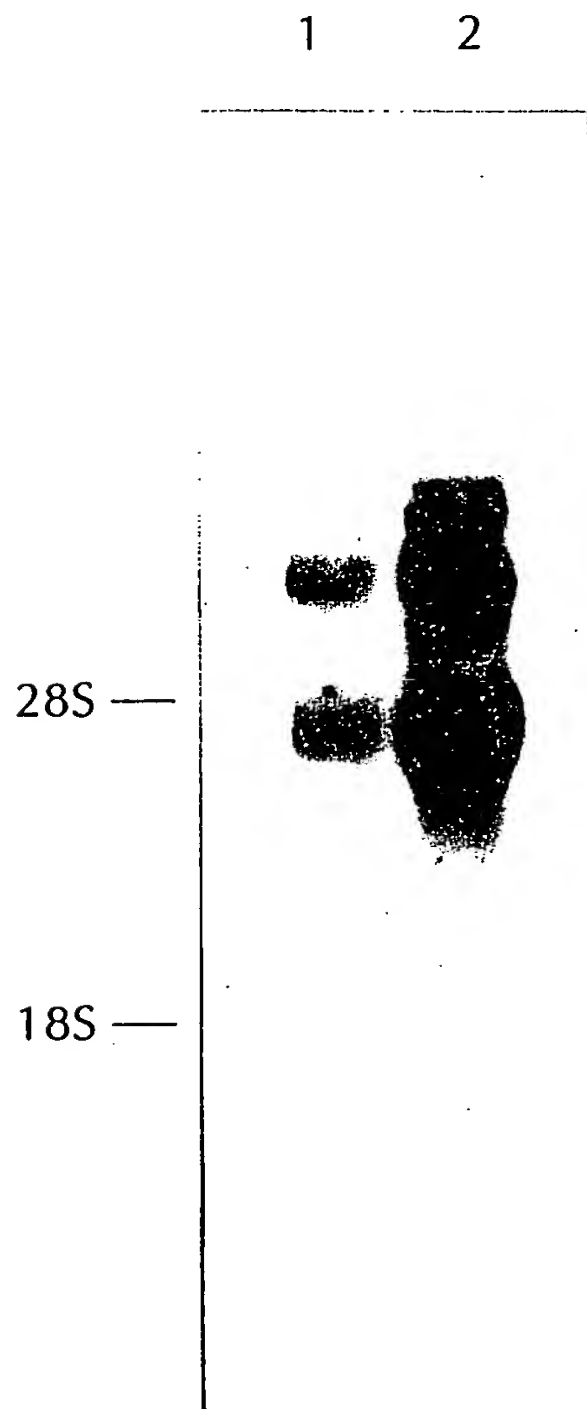


FIG. 12B

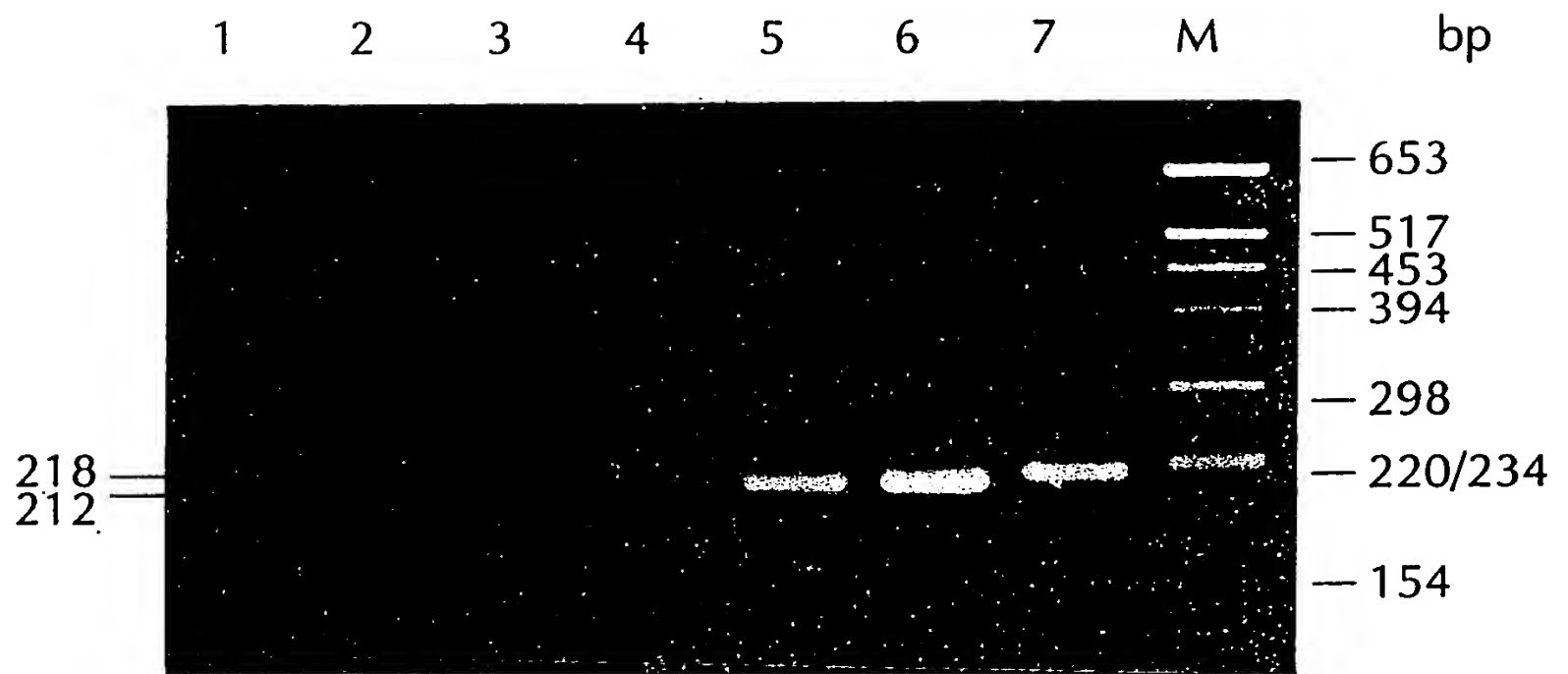


FIG. 12C

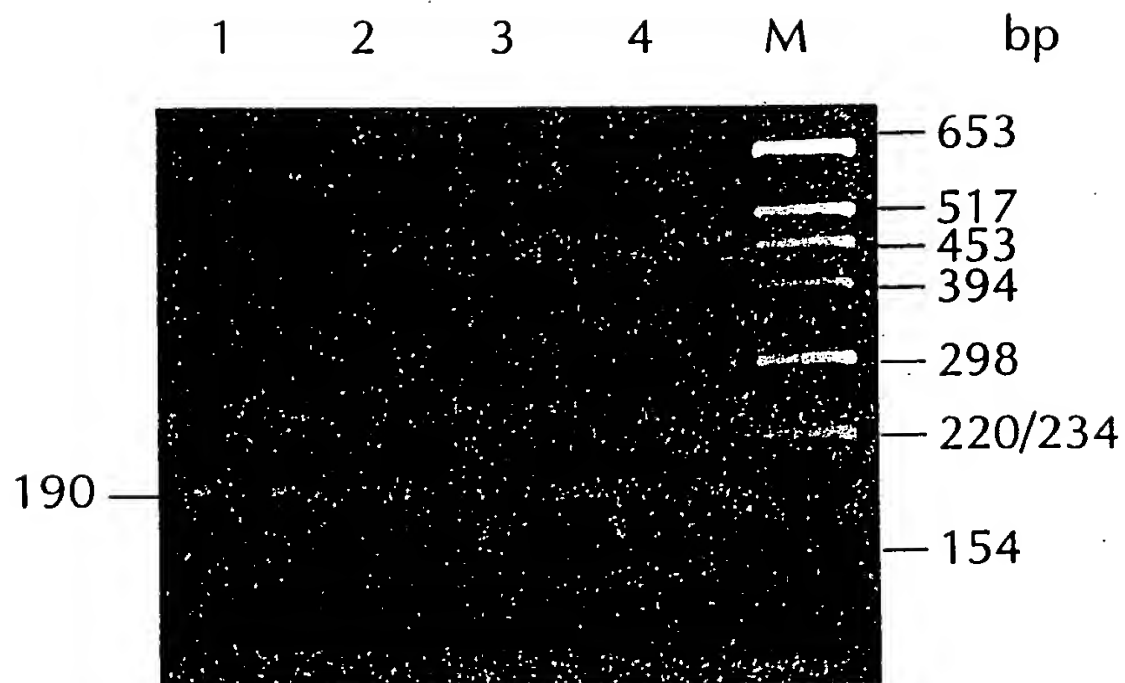


FIG. 13A

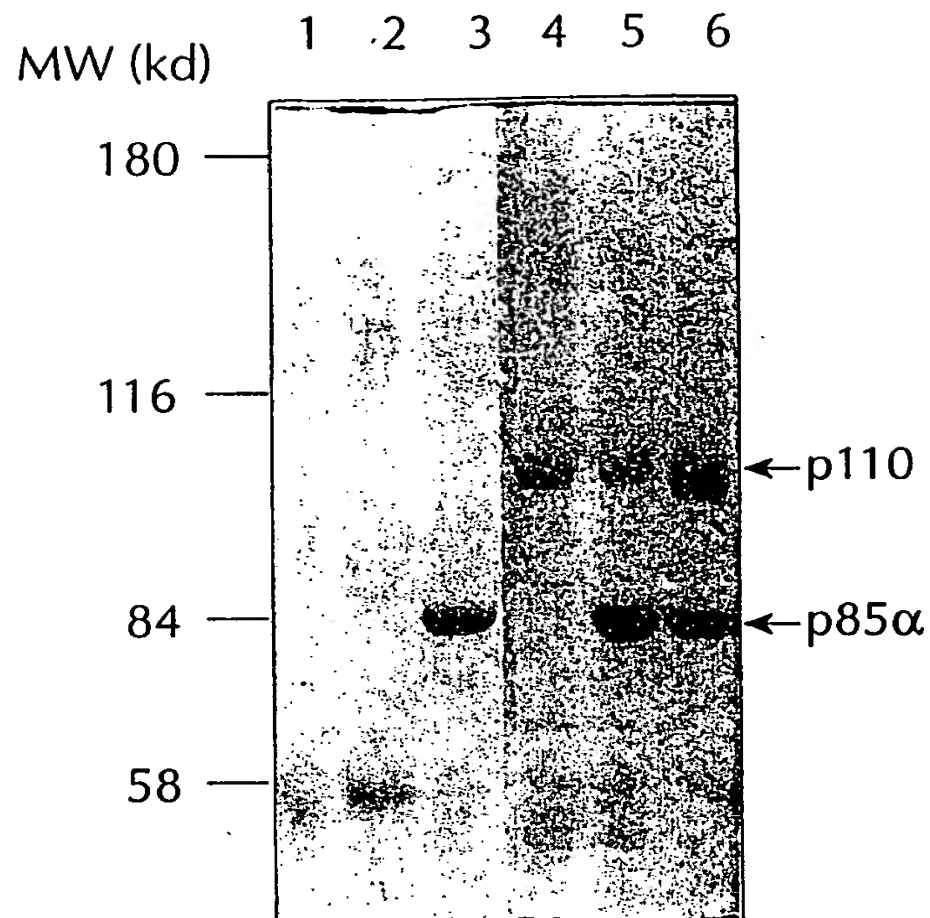


FIG. 13B

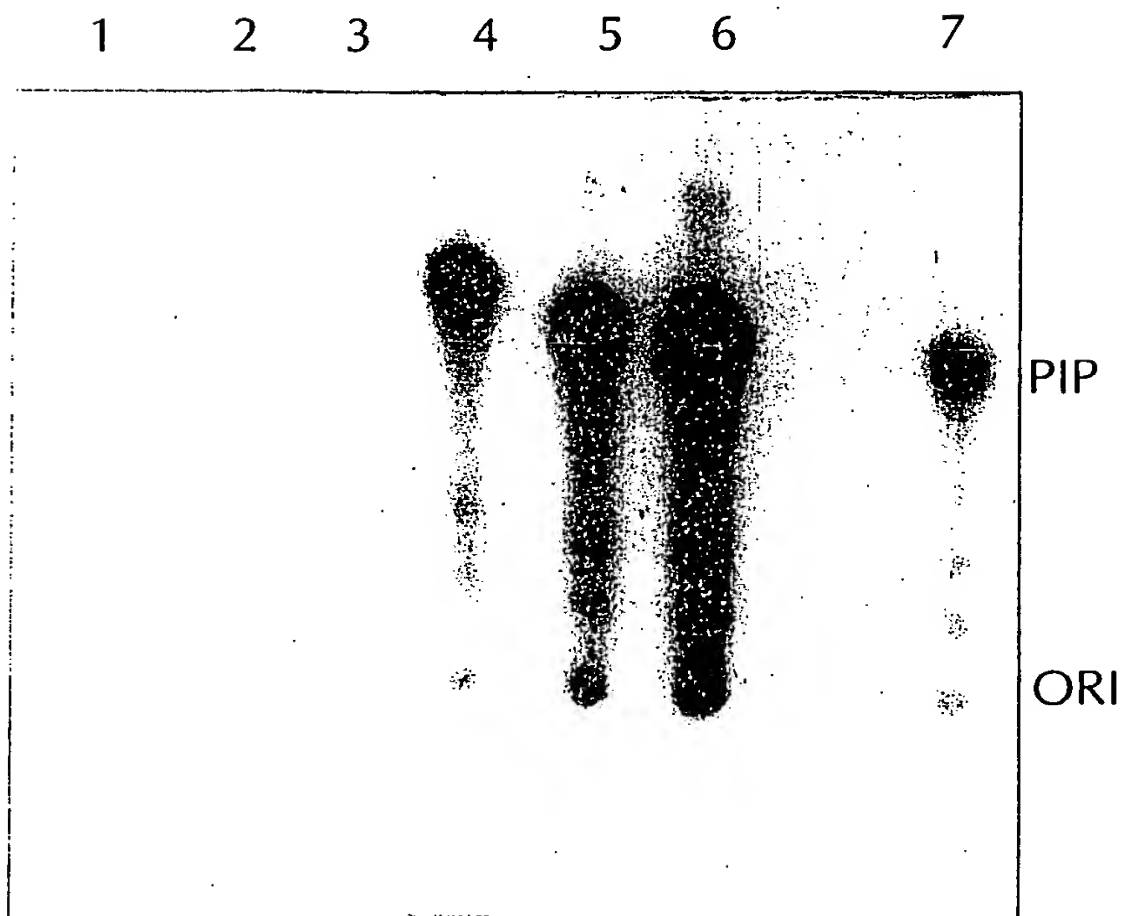


FIG. 14A

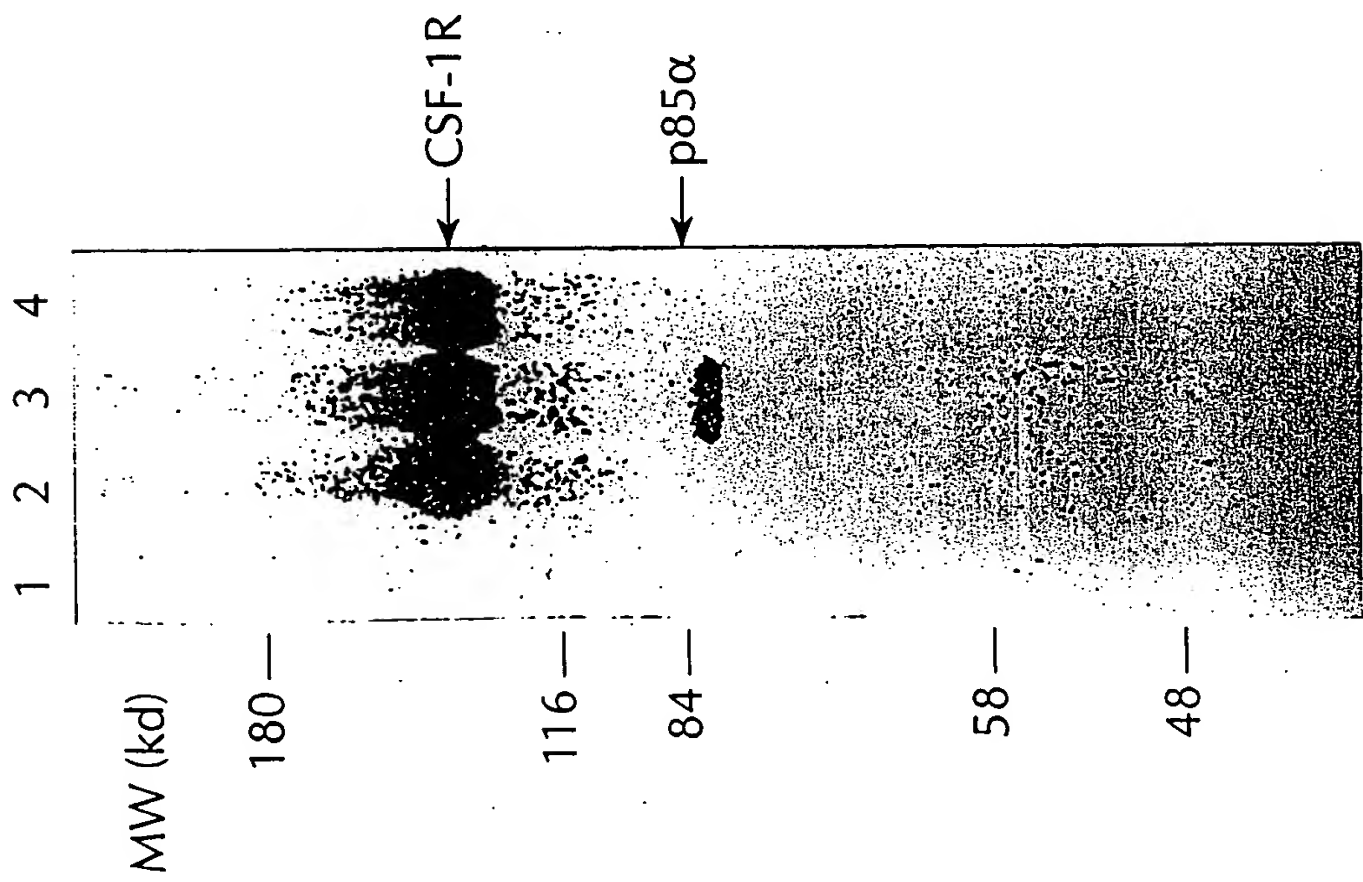


FIG. 14B

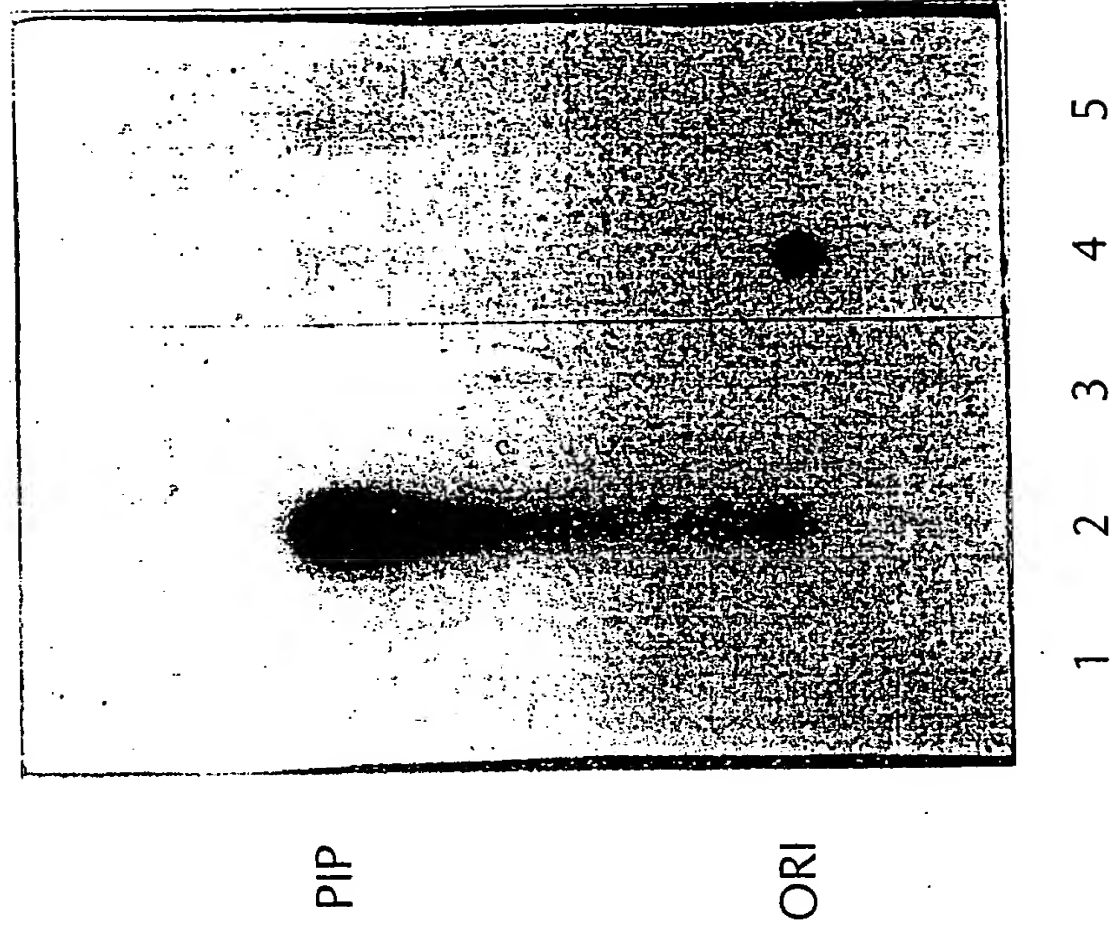


FIG. 15A

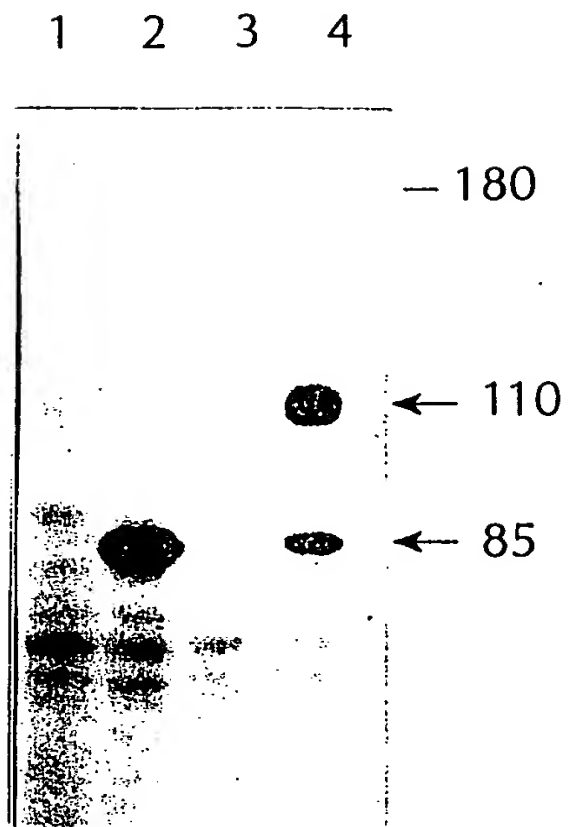


FIG. 15B

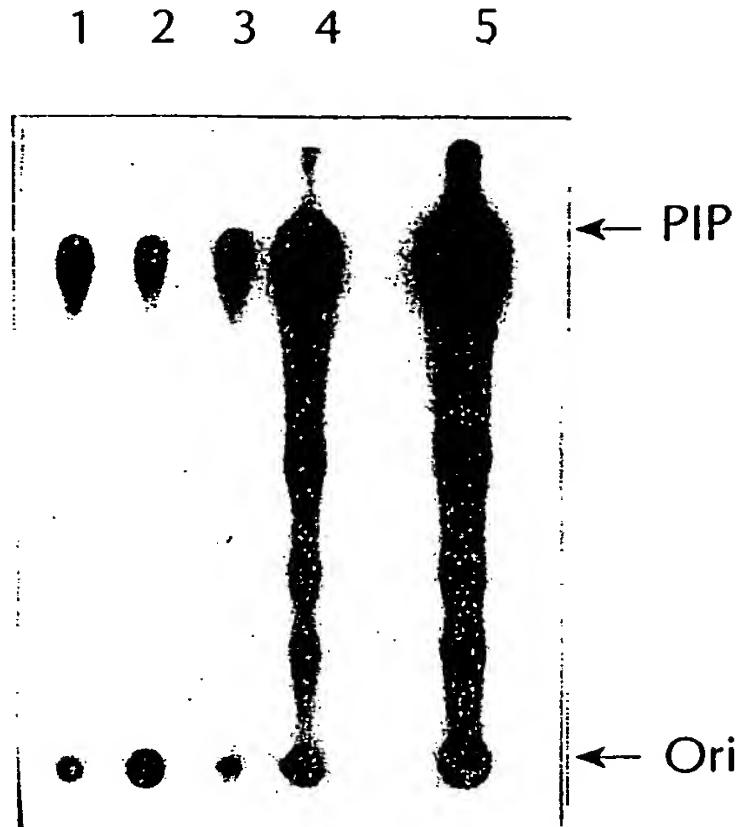


FIG. 15C

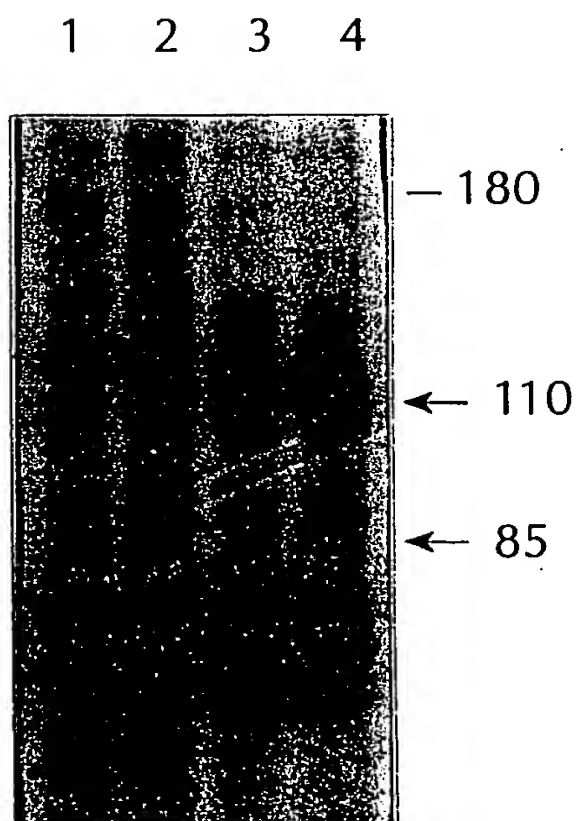


FIG. 15D

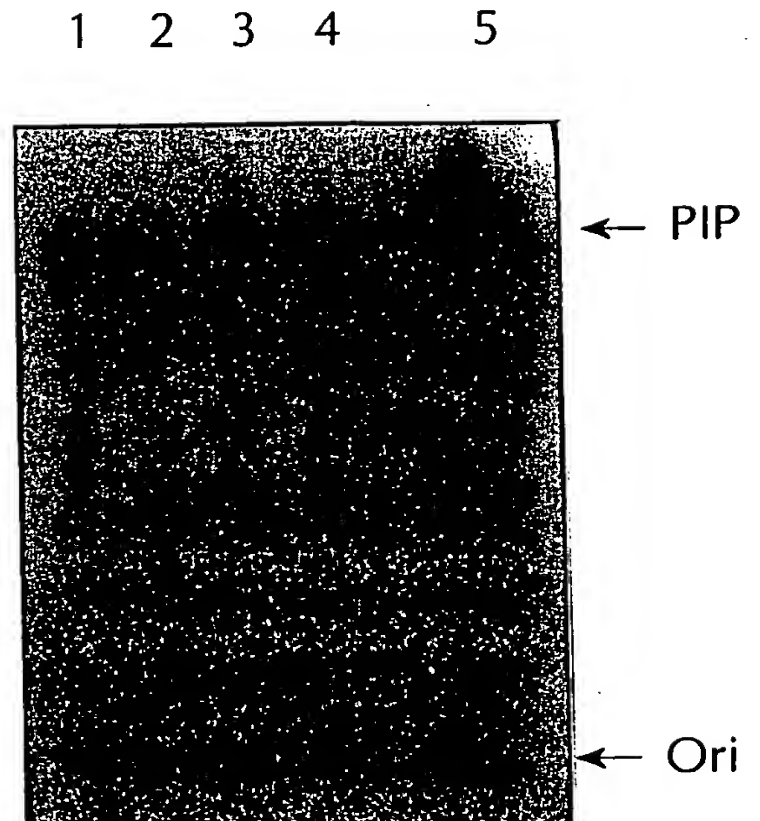


FIG. 16A

1 ATGCCCTCCAAGACCATCATCAGGTGAACGTGGGGCATCCACTTGATG 48
-----+-----+-----+-----+-----+-----
TACGGAGGTTCTGGTAGTAGTCCACTTGACACCCCCGTAGGTGAACACTAC
M P P R P S S G E L W G I H L M
49 CCCCCAAGAATCCTAGTGGAATGTTTACTACCAAAATGGAATGATAGTG 96
-+-----+-----+-----+-----+-----+-----
GGGGTCTTAGGATCACCTTACAAATGATGGTTTACCTTACTATCAC
P P R I L V E C L L P N G M I V
97 ACTTTAGAATGCCCTCCGTGAGGCTACATTAGTAATAAGCATGAA 144
---+-----+-----+-----+-----+-----+-----
TGAAATCTTACGGAGGCACTCCGATGTAATCATTGATATTCGTACTT
T L E C L R E A T L V T I K H E
145 CTATTAAAGAAGCAAGAAATACCCCTCTCCATCAACTTCTCAAGAT 192
-----+-----+-----+-----+-----+-----+-----
GATAAATTCTTCGTTCTTTTATGGGAGAGGTAGTTGAAGAAGTTCTA
L F K E A R K Y P L H Q L L Q D

FIG. 16B

193 GAATCTTCTTACATTTTCGTAAGTGTTACCCAGAAGCAGAAAGGGAA
-----+-----+-----+-----+-----+
CTTAGAAGATGTAAAGCATTCACAATGGGTTCTTCGTCCTTCCCTT
E S S Y I F V S V T Q E A E R E 240

241 GAATTTTGTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAA
-----+-----+-----+-----+-----+
CTTAAAAAATACTTTGTTCTGCTGAAACACTAGAACCCGAAAAAGTT
E F F D E T R R L C D L R L F Q 288

289 CCATTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAAGAAAGATC
--+-----+-----+-----+-----+-----+
GGTAAAAAATTTTCATTAACTTGGTCATCCGTTGGCACTTCTTTCTAG
P F L K V I E P V G N R E E K I 336

337 CTCATCGAGAAATTGGTTTGTCTATCGGCATGCCAGTGTCGAATT
--+-----+-----+-----+-----+-----+
GAGTTAGCTCTTTAAACCAAAACGATAGCCGTACGGTCACACGCTTAAA
L N R E I G F A I G M P V C E F 384

FIG. 16C

385 GATATGGTTAAAGATCCTGAAGTACAGGACTTCCGAAGAAATATCTT
-----+-----+-----+-----+-----+-----+-----
CTATACCAATTCTAGGACTTCAATGTCCTGAAGGCTTCTTTATAAGAA
D M V K D P E V Q D F R R N I L
432

433 AATGTTGTAAAGAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT
-----+-----+-----+-----+-----+-----+-----
TTACAAACATTTCTCGACACCTAGAAATCCCTAGAAATTAAGTGGAGTA
N V C K E A V D L R D L N S P H
480

481 AGTAGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAG
-----+-----+-----+-----+-----+-----+-----
TCATCTCGTTACATACAGATAGCGGTGTACATCTTAGAAGTGGTCTC
S R A M Y V Y P P H V E S S P E
528

529 CTGCCAAGCACATATATAATAAATTGGATAGAGGCCAAATAATAGTG
-+-----+-----+-----+-----+-----+-----+-----
GACGGTTTCGTATATATTTAACCTATCTCCGGTTTATATATCAC
L P K H I Y N K L D R G Q I I V
576

FIG. 16D

577 GTGATTGGGTAATAGTTTCTCCAAATAATGACAAGCAGAGTATACT
624 - - - - - + - - - - - + - - - - - + - - - - - + - - - - -
CACTAAACCCATTATCAAGAGGTTTATTACTGTTCGCTTCATATGA
V I W V I V S P N N D K Q K Y T
672 CTGAAATCAACCATGACTGTGTGCCAGAACAAAGTAATTGCTGAAGCA
- - - - - + - - - - - + - - - - - + - - - - - + - - - - -
GACTTTAGTTGGTACTGACACACGGTCTTGTTCATTAACGACTTCGT
L K I N H D C V P E Q V I A E A
720 ATCAGGAAAAAATAAGTAATGTGCTATCATCTGAACAATTAAAA
- - - - - + - - - - - + - - - - - + - - - - - + - - - - -
TAGTCCCTTTTGTGATCTTCATACAACGATAGTAGACTTGTAAATTT
I R K K T R S M L L S S E Q L K
768 CTCGTGTTTATAGATATCAGGGCAAGTACATTTTAAAGTGTGTGGA
- - - - - + - - - - - + - - - - - + - - - - - + - - - - -
GAGACAAAAATCTTATAGTCCCGTTCATGTAAATTTTCACACACCT
L C V L E Y Q G K Y I L K V C G

FIG. 16E

| | | |
|-----|--|-----|
| 769 | TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTAT +-----+-----+-----+-----+-----+-----+ ACACTATTATGAAGGATCTTTTATAGGAGACTCAGTCATATTCATA C D E Y F L E K Y P L S Q Y K Y | 816 |
| 817 | ATAAGAAGCTGTATAATGCTTGGAGGATGCCCAATTGAAGATGATG +-----+-----+-----+-----+-----+-----+ TATTCTTCGACATATTACGAACCCCTCCTACGGTTAAACTTCTACTAC I R S C I M L G R M P N L K M M | 864 |
| 865 | GCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGACTGTTTACAATG +-----+-----+-----+-----+-----+-----+ CGATTTCTTCGGAAATAAGAGTTGACGGTTACCTGACAAAATGTTAC A K E S L Y S Q L P M D C F T M | 912 |
| 913 | CCATCTTATCCAGACGCATTTCCACAGCTACACCATATATGAATGGA +-----+-----+-----+-----+-----+-----+ GGTAGAATAAGGCTGCGTAAAGGTGTCGATGTGGTATATACTTACCT P S Y S R R I S T A T P Y M N G | 960 |

FIG. 16F

```
961      GAAACATCTACAATAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA
      -----+-----+-----+-----+-----+-----
      CTTGTAGATGTTTAGGAAACCCAATATTATCTCGTGAGTCTTAT
      E T S T K S L W V I N R A L R I
1008

1009     AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGAC
      -+-----+-----+-----+-----+-----+-----
      TTTAAGAAACACGTTGGATGCACCTTAGATTATAAGCTCTGTAACTG
      K I L C A T Y V N L N I R D I D
1056

1057     AAGATTATGTTCCGAACAGGTATCTACCATGGAGGAGAACCCCTTATGT
      ---+-----+-----+-----+-----+-----+-----
      TTCTAAATACAAGCTTGTCCATAGATGGTACCTCCTCTTGGGAATACA
      K I Y V R T G I Y H G G E P L C
1104

1105     GACAATGTGAACACTCAAGAGTACCTTGTTCCAATCCCAGGTGGAAT
      -----+-----+-----+-----+-----+-----+-----
      CTGTTACACTTGTGAGTTTCTCATGGAACAAGGTTAGGGTCCACCTTA
      D N V N T Q R V P C S N P R W N
1152
```

FIG. 16G

1153 GAATGGCTGAATTATGATATATACATTCTCTGATCTTCTCTGCTGCTGCT
-----+-----+-----+-----+-----+-----+
CTTACCGACTTAATACTATATATGTAAGGACTAGAGGAGCAGCAGACGA
E W L N Y D I Y I P D L P R A A 1200

1201 CGACTTTGCCCTTCCATTGCTCTCTGTTAAAGGCCGAAAGGGTGCTAAA
-----+-----+-----+-----+-----+-----+
GCTGAAACGGAAAGGTAAACGAGACAAATTCCGGCTTCCACGATTT
R L C L S I C S V K G R K G A K 1248

1249 GAGGAACACTGTCCATTGGCATGGGGAATAATAAACTTGTGATTAC
-----+-----+-----+-----+-----+-----+
CTCCTTGTGACAGGTAACCGTACCCCTTTATATTTGAACAACCTAATG
E E H C P L A W G N I N L F D Y 1296

1297 ACAGACACTCTAGTATCTGGAAAATGGCTTTGAATCTTTGGCCAGTA
-----+-----+-----+-----+-----+-----+
TGTCGTGAGATCATAGACCTTTTACCAGAACTTAGAAACCGGTCAT
T D T L V S G K M A L N L W P V 1344

| | | |
|------|---|------|
| 1345 | CCTCATGGATTAGAAGATTGCTGAACCCCTATTGGTGTACTGGATCA - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - GGAGTACCTAATCTTCTAAACGACTTGGGATAACCAACAATGACCTAGT P H G L E D L L N P I G V T G S | 1392 |
| 1393 | AATCCAAATAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - TTAGGTTTATTTCTTGAGGTACGAATCTCAACCTCAAACTGACCAAG N P N K E T P C L E L E F D W F | 1440 |
| 1441 | AGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - TCGTCAACCATTTCAAGGGTCTATACAGTCACTAACTTCTCGTACGG S S V V K F P P D M S V I E E H A | 1488 |
| 1489 | AATTGGTCTGTATCCCGAGAAGCAGGATTAGCTATTCCCACGCAGGA - + - - - - - - - - - + - - - - - + - - - - - + - - - - - + - - - - - TTAACCAACATAGGGCTCTTCGTCCCTAAATCGATAAGGTGCGTCCT N W S V S R E A G F S Y S H A G | 1536 |

FIG. 16I

| | | |
|------|--|------|
| 1537 | CTGAGTAACAGACTAGCTAGAGACAATGAATTAAGGGAAAATGACAAA -----+-----+-----+-----+-----+----- GACTCATTTGCTGATCGATCTCTGTACTTAATTCCTTTTACTGTTT L S N R L A R D N E L R E N D K | 1584 |
| 1585 | GAACAGCTCAAAGCAATTCTACACGAGATCCTCTCTCTGAAATCACT -----+-----+-----+-----+-----+----- CTGTCGAGTTTCGTTAAAGATGTGCTCTAGGAGAGACTTTAGTGA E Q L K A I S T R D P L S E I T | 1632 |
| 1633 | GAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAAC -----+-----+-----+-----+-----+----- CTCGTCCCTCTTTCTAAAGATACTCAGTGTCTGTGATAACACATTGA E Q E K D F L W S H R H Y C V T | 1680 |
| 1681 | ATCCCCGAAATTCTACCCCAAATTGCTTCTGTCTGTAAATGGAATTCT -----+-----+-----+-----+-----+----- TAGGGGCTTTAAGATGGGTTTAACGAAGACAGACAAATTACCTTAAGA I P E I L P K L L L S V K W N S | 1728 |

FIG. 16

| | | |
|------|--|------|
| 1729 | AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAGATTGGCCTCCA | 1776 |
| | -+-----+-----+-----+-----+-----+----- | |
| | TCTCTACTTCATCGGTCTACATAACGAACCATTTTCTAACCGAGGT | |
| | R D E V A Q M Y C L V K D W P P | |
| 1777 | ATCAAACCTGAACAGGCTATGGAACTTCTGGACTGTAATTACCCAGAT | 1824 |
| | ---+-----+-----+-----+-----+-----+----- | |
| | TAGTTTGACTTGTCGGATACCTTGAAGACCTGACATTAATGGGTCTA | |
| | I K P E Q A M E L L D C N Y P D | |
| 1825 | CCTATGGTTCGAGGTTTGTGCTGCTTCGGTGCTTGGAATAATTTAACA | 1872 |
| | ---+-----+-----+-----+-----+-----+----- | |
| | GGATACCAAGCTCCAACGACAAGCCACGAACCTTTTATATAAATTGT | |
| | P M V R G F A V R C L E K Y L T | |
| 1873 | GATGACAACTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA | 1920 |
| | ---+-----+-----+-----+-----+-----+----- | |
| | CTACTGTTGAAAGAGTCATAAATTAAAGTCGATCATGTCCAGGATTTT | |
| | D D K L S Q Y L I Q L V Q V L K | |

FIG. 16K

| | | |
|------|--|------|
| 1921 | TATGAACAATATTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA -----+-----+-----+-----+-----+----- ATACTGTTATAAACCTATTGAACGAACACTCTAAAAATGACTTCTTT Y E Q Y L D N L L V R F L L K K | 1968 |
| 1969 | GCATTGACTAATCAAGGATTGGGCACCTTTTCTTTTGGCATTTAAAA -+-----+-----+-----+-----+-----+----- CGTAACTGATTAGTTTCTAACCCTGAAAGAAACCGTAAATTTT A L T N Q R I G H F F F W H L K | 2016 |
| 2017 | TCTGAGATGCACAATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTG -----+-----+-----+-----+-----+----- AGACTCTACGTGTTATTTTGTCAATCGGTCTCCAAACCGGACGAAAC S E M H N K T V S Q R F G L L L | 2064 |
| 2065 | GAGTCCTATTGTCGTGCATGTGGGATGTATTGAAGCACCTGAATAGG -----+-----+-----+-----+-----+----- CTCAGGATAACAGCACGTACACCCCTACATAAACTTCGTGGACTTATCC E S Y C R A C G M Y L K H L N R | 2112 |

FIG. 16L

| | | |
|------|--|------|
| 2113 | CAAGTCGAGGCAATGGAAAAGCTCATTAACCTTAACCTGACATTTCTCAAA -----+-----+-----+-----+-----+-----+ GTCAGCTCCGTTACCTTTTCGAGTAATTGAATTGACTGTAAGAGTTT Q V E A M E K L I N L T D I L K | 2160 |
| 2161 | CAGGAGGAAGGATGAACAACAAAAGGTACAGATGAAGTTTTAGTT -----+-----+-----+-----+-----+-----+ GTCCTCTCCTTCCCTACTTTGTGTTTCCATGTCTACTTCAAAAATCAA Q E R K D E T Q K V Q M K F L V | 2208 |
| 2209 | GAGCAAATGAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTG --+-----+-----+-----+-----+-----+-----+ CTCGTTTACTCCGCTGGTCTAAAGTACCTACGGGATGTCCCGAACGAC E Q M R R P D F M D A L Q G L L | 2256 |
| 2257 | TCTCCTCTAAACCCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAG ---+-----+-----+-----+-----+-----+-----+ AGAGGAGATTGGGACGAGTAGTTGATCCTTTGGAGTCCGAATTTC S P L N P A H Q L G N L R L K E | 2304 |

FIG. 16M

2305 TGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGGAG
-----+-----+-----+-----+-----+-----+-----+
ACAGCTTAATACAGAAGACGTTTTCCTCGGTGACACCAACTTAACCCCTC
C R I M S S A K R P L W L N W E
2352

2353 AACCCAGACATCATGTCAGAGTTACTGTTTCAGAACAAATGAGATCATC
-----+-----+-----+-----+-----+-----+-----+
TTGGGTCTGTAGTACAGTCTCAATGACAAAGTCTTGTTACTCTAGTAG
N P D I M S E L L F Q N N E I I
2400

2401 TTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATT
-----+-----+-----+-----+-----+-----+-----+
AAATTTTACCCCTACTAAATGCCGTTCTATACGATTGTGAAGTTTAA
F K N G D D L R Q Q D M L T L Q I
2448

2449 ATTCGTATTATGGAAATACTGGCAAAATCAAGTCTTGATCTTCGA
-----+-----+-----+-----+-----+-----+-----+
TAAGCATAATACCTTTTATAGACCGTTTTAGTTCAGAACTAGAAGCT
I R I M E N I W Q Q N Q G L D L R
2496

FIG. 16N

2497 ATGTTACCTTATGGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATT
-----+-----+-----+-----+-----+-----
TACAATGGAATACCAACAGACAGTTAGCCACTGACACACCCCTGAATAA
M L P Y G C L S I G D C V G L I
2544

2545 GAGGTGGTCCGAAATTCTCACACTATTATGCAAAATTCAGTGCAAAGGC
-----+-----+-----+-----+-----+-----+-----
CTCCACCACGCTTTAAGAGTGTGATAATACGTTTAAGTCACGTTTCCG
E V V R N S H T I M Q I Q C K G
2592

2593 GGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGG
-----+-----+-----+-----+-----+-----+-----
CCGAACTTTCACGTGACGTCAAGTTGTCGGTGTGTGATGTAGTCACC
G L K G A L Q F N S H T L H Q W
2640

2641 CTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCCTG
-----+-----+-----+-----+-----+-----+-----
GAGTTTCTGTCTTGTTCCTCTTTATATATACTACGTCGGTAACTGGAC
L K D K N K G E I Y D A A I D L
2688

+

| | | |
|------|--|------|
| 2881 | TTAATAGTGATTAGTAAAGGAGCCCAAGAAATGCACAAAGACAAGAGAA -----+-----+-----+-----+-----+----- AATTATCACTAATCATTTCTCGGTTCTTACGTGTTTCTGTCTCTT L I V I S K G A Q E C T K T R E | 2928 |
| 2929 | TTTGAGAGGTTTCAGGAGATGTGTACAAGGCTTATCTAGCTATTCTGA -+-----+-----+-----+-----+-----+----- AAACTCTCCAAAGTCTCTACACAATGTTCGGAATAGATCGATAAGCT F E R F Q E M C Y K A Y L A I R | 2976 |
| 2977 | CAGCATGCCAATCTCTTCATAAAATCTTTTCTCAATGATGCTTGGCTCT ---+-----+-----+-----+-----+-----+----- GTCGTACGGTTAGAGAAGTATTTAGAAAAGAGTTACTACGAACCGAGA Q H A N L F I N L F S M M L G S | 3024 |
| 3025 | GGAATGCCAGAACTACAATCTTTTGATGACATTGCATACATTCGAAAG -----+-----+-----+-----+-----+-----+----- CCTTACGGTCTTGATGTTAGAAAACACTACTGTAAACGTATGTAAAGCTTTC G M P E L Q S F D I A Y I R K | 3072 |

+

FIG. 16Q

| | | |
|------|--|------|
| 3073 | ACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATG -----+-----+-----+-----+-----+-----+-----+ TGGGATCGGAATCTATTTTGGACTCGTTCTCCGAAACCTCATAAAGTAC T L A L D K T E Q E A L E Y F M | 3120 |
| 3121 | AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAATGGAT -----+-----+-----+-----+-----+-----+-----+ TTTGTTTACTTACTACGTGTAGTACCACCGACCTGTGTTTTTTACCTA K Q M N D A H H G G W T T K M D | 3168 |
| 3169 | TGGATCTTCCACACAATTAAACAGCATGCATTGAACCTGAAAGATAACT -+-----+-----+-----+-----+-----+-----+-----+ ACCTAGAAGGTGTGTTAATTGTCGTACGTAACTTGACTTTCCTATTGA W I F H T I K Q H A L N * | 3216 |
| 3217 | GAGAAAATGAAAGCTCACTCTGGATTCCACACTGCACCTGTTAATAACT ---+-----+-----+-----+-----+-----+-----+-----+ CTCTTTTACTTTCGAGTGAGACCTAAGGTGTGACGTGACAAATTATTGA | 3264 |

+

+

| | | |
|------|---|------|
| 3265 | CTCAGCAGGCAAGACCGATTGCATAGGAATTGCACAATCCATGAACA | 3312 |
| | -----+-----+-----+-----+-----+----- | |
| | GAGTCGTCGTTTCTGGCTAACGTATCCTTAACGTGTAGGTACTTGT | |
| 3313 | GCATTAGATTACAGCAAGAACAGAAATAAAATACATATAATTAA | 3360 |
| | -----+-----+-----+-----+-----+----- | |
| | CGTAATCTAAATGTCGTTCTTGTCTTTATTTATGATATATAAATT | |
| 3361 | TAAATGTAAACGCAAAACAGGGTTTGATAGCACTTAAACTAGTTCATTC | 3408 |
| | -----+-----+-----+-----+-----+----- | |
| | ATTACATTGCGTTTGTCCCAAACTATCGTGAATTGATCAAGTAAAG | |
| 3409 | AAAA | |
| | -+-- | 3412 |
| | TTTT | |

FIG. 17A

hum110 1 ATGCCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCC 50
|||||
bov110 1 ATGCCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCC 50
51 CCCAAGAATCCTAGTGGAATGTTTACTACCAAAATGGAATGATAGTGACTT 100
|||||
51 CCCAAGAATCCTAGTAGAATGTTTACTACCAAAATGGGATGATAGTGACTT 100
101 TAGAATGCCCTCCGTGAGGCTACATTAGTAACATAAAGCATGAACATAATT 150
|||||
101 TAGAATGCCCTCCGTGAGGCTACGTTAATAACGATAAAGCATGAACATAATT 150
151 AAAGAAGCAAGAAAATACCCCTCTCCATCAACTTCTTCAAGATGAATCTTC 200
|||||
151 AAAGAAGCAAGAAAATACCCCTCTCCATCAACTTCTTCAAGATGAATCTTC 200

FIG. 17B

201 TTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAAGAAATTTTTCG 250
|||||
201 TTACATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAAGAAATTTTTCG 250
|||||
251 ATGAAACAAGACGACTTTGTGATCTTCGGCTTTTCAACCAATTTTAAAA 300
|||||
251 ATGAAACAAGACGACTTTGTGACCTTCGGCTTTTCAACCCCTTTTAAAA 300
|||||
301 GTAATTGAACCAAGTAGGCAACCGTGAGAAAGATCCTCAATCGAGAAAT 350
|||||
301 GTAATTGAACCAAGTAGGCAACCGTGAGAAAGATCCTCAATCGAGAAAT 350
|||||
351 TGGTTTGTCTATCGGCATGCCAGTGTCGGAATTTGATATGTTAAAGATC 400
|||||
351 TGGTTTGTCTATCGGCATGCCAGTGTCGGAATTCGATATGTTAAAGATC 400
|||||
401 CTGAAGTACAGGACTTCCGAAGAAATATCTTAATGTTTGTAAAGAAGCT 450
|||||
401 CAGAAGTACAGGACTTCCGAAGAAATATCTCAATGTTTGTAAAGAAGCT 450
|||||

FIG. 17C

451 GTGGATCTTAGGGATCTTAATTACCTCATAGTAGCAATGTATGTCTA 500
|||||
451 GTGGATCTTAGGGATCTTAATTACCTCATAGTAGCAATGTATGTCTTA 500
501 TCCGCCACATGTAGAACTTTCACCAGAGCTGCCAAAGCACATATAATA 550
|||
501 TCCTCCAAATGTAGAACTTTCACCAGAACTGCCAAAGCACATATAATA 550
551 AATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTAATAGTTTCTCCA 600
|||||
551 AATTGGATAAAGGGCAATAATAGTGGTGATTGGGTAATAGTTTCTCCA 600
601 AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCC 650
|||||
601 AATAATGACAACAGAAAGTATACTCTGAAAATCAACCATGACTGTGTGCC 650
651 AGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGC 700
|||||
651 AGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGC 700

FIG. 17D

701 TATCATCTGAACAATTAAAACTCTGTGTTTGAATAATCAGGCAAGTAC 750
|||||
701 TATCATCTGAACAACATAAACTCTGTGTTTGAATAATCAGGCAAGTAT 750
751 ATTTAAAGTGTGGATGTGATGAATACTTCTAGAAATAATCCTCT 800
|||||
751 ATTTAAAGTGTGGATGTGATGAATACTTCTAGAAATAATCCTCT 800
801 GAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGAGGATGCCCA 850
|||||
801 GAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTTGGAGGATGCCCA 850
851 ATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC 900
|||||
851 ATTTGATGCTGATGGCTAAAGAAAGCCTCTATTCTCAACTGCCAATGGAC 900
901 TGTTTACAATGCCATCTTATTCAGACGCATTTCACAGCTACACCATA 950
|||||
901 TGTTTACAATGCCATCATATTCAGACGCATCTCCACAGCTACGCCATA 950

FIG. 17E

951 TATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCAC 1000
|||||
951 TATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGAC 1000
|||||
1001 TCAGAAATAAAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGAC 1050
|||||
1001 TCAGAAATAAAAATTCTTTGTGCAACCTATGTGAATGTAAATATTCGAGAC 1050
|||||
1051 ATTGACAAGATTATGTTCGAACAGGTATCTACCATGGAGAGAACCCCTT 1100
|||||
1051 ATTGACAAGATTATGTTCGAACAGGTATCTACCATGGAGAGAACCCCTT 1100
|||||
1101 ATGTGACAAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGA 1150
|||||
1101 ATGTGATAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGA 1150
|||||
1151 ATGAATGGCTGAATTATGATATATACATTCCCTGATCTTCCTCGTGCTGCT 1200
|||||
1151 ATGAATGGCTGAATTACGATATATACATTCCCTGATCTTCCTCGTGCTGCT 1200
|||||

FIG. 17F

1201 CGACTTTGCCCTTTCCATTGCTCTGTTAAAGGCCGAAAGGGTGCTAAAGA 1250
|||||
1201 CGACTTTGCCCTTTCCATTGTTCTGTTAAAGGCCGAAAGGGTGCTAAAGA 1250
|||||
1251 GGAACACTGTCCATTGGCATGGGAAATATAAATTGTTGATTACACAG 1300
|||||
1251 GGAACACTGTCCATTGGCCTGGGAAATATAAATTGTTGATTACACAG 1300
|||||
1301 AACTCTAGTATCTGGAAATAATGGCTTTGAATCTTTGGCCAGTACCTCAT 1350
|||||
1301 ATACTCTAGTATCTGGAAATAATGGCTTTGAATCTTTGGCCAGTACCTCAT 1350
|||||
1351 GGATTAGAAGATTTGCTGAACCCCTATTGGTGTACTGGATCAAATCCAAA 1400
|||||
1351 GGACTAGAAGATTTGCTGAACCCCTATTGGTGTACTGGATCAAATCCAAA 1400
|||||
1401 TAAAGAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTCAGCAGTGTGG 1450
|||||
1401 TAAAGAACTCCATGTTTAGAGTTGGAGTTTGACTGGTTCAGCAGTGTGG 1450
|||||

FIG. 17G

1451 TAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCCAAATTGGTCTGTA 1500
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1451 TAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCCAAATTGGTCTGTA 1500

1501 TCCCGAAGCAGGATTTAGCTATTCCACGCAGGACTGAGTAACAGACT 1550
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1501 TCCCGTGAAGCAGGATTTAGTTATTCCCATGCAGGACTGAGTAACAGACT 1550

1551 AGCTAGAGACAAATGAATTAAGGGAATAAGACAAAGACAGCTCAAAGCAA 1600
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1551 AGCTAGAGACAAATGAATTAAGAGAAATAATGATAAAGAACAGCTCCGAGCAA 1600

1601 TTTCTACACGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTT 1650
||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1601 TTTGTACACGAGATCCTCTATCTGAAATCACTGAGCAAGAGAAAGATTTT 1650

1651 CTATGGAGTCACAGACACTATTGTGTAACTATCCCCGAAATTTCTACCCAA 1700
|| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1651 CTGTGGAGCCACAGACACTATTGTGTAACTATCCCCGAAATTTCTACCCAA 1700

FIG. 17H

1701 ATTGCTTCTGCTGTAAATGGAATTCTAGAGATGAAGTAGCCAGATGT 1750
|||||
1701 ATTGCTTCTGCTGTAAATGGAACTCTAGAGATGAAGTAGCTCAGATGT 1750

1751 ATTGCTTGGTAAAGATTGGCCTCCAATCAACCTGAACAGGCTATGGAA 1800
|
1751 ACTGCTTGGTAAAGATTGGCCTCCAATCAAGCCTGAACAGGCTATGGAG 1800

1801 CTTCTGGACTGTAAATTACCCAGATCCTATGGTTCGAGGTTTGTGCTGTTCTG 1850
|||||
1801 CTTCTGGACTGCAATTACCCAGATCCTATGGTTCGAGGTTTGTGCTGTTCTG 1850

1851 GTGCTTGGAAATAATTTAACAGATGACAAACTTCTCAGTATTTAATTC 1900
|||||
1851 GTGCTTAGAAATAATTTAACAGATGACAAACTTCTCAGTACCTAATTC 1900

1901 AGCTAGTACAGGTCCTAAATAATGAACAATAATTGGATAACTTGCTTGTG 1950
|||||
1901 AGCTAGTACAGGTACTAAATAATGAACAGTATTTGGATAACCTGCTTGTG 1950

FIG. 17I

1951 AGATTTTACTGAAGAACATTGACTAATCAAAGGATTGGGCACCTTTT 2000
|||||
1951 AGATTTTACTCAAAAAGCGTTAACTAATCAAAGGATCGGTCACCTTTT 2000
2001 CTTTGTGGCATTAAATCTGAGATGCACAAATAAAACAGTTAGCCAGAGGT 2050
|||||
2001 CTTTGTGGCATTAAATCTGAGATGCACAAATAAAACAGTTAGTCAGAGGT 2050
2051 TTGGCCTGCTTTTGGAGTCCTATTGTCGTGCATGTGGGATGTATTGAAG 2100
|||||
2051 TTGGCCTGCTTTTGGAGTCCTATTGCCGTGCATGTGGGATGTATCTGAAG 2100
2101 CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAAGTGA 2150
|||||
2101 CACCTTAATAGGCAAGTTGAGGCTATGGAAAAGCTCATTAACCTGACTGA 2150
2151 CATTCTCAACAGGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGT 2200
|||||
2151 CATTCTCAACAGAGAGGAAGGATGAAACACAAAAGGTACAGATGAAGT 2200

FIG. 17J

2201 TTTTAGTGAGCAAAATGAGCGGACCAGATTTCATGGATGCCCTACAGGGC 2250
|||||
2201 TTTTAGTGAGCAAAATGCGCGGACCAGATTTCATGGATGCTCTCCAGGGC 2250
2251 TTGCTGTCTCCTCTAAACCCCTGCTCATCAACTAGGAAACCTCAGGCTTAA 2300
||
2251 TTTCTGTCTCCTCTAAACCCCTGCTCATCAGCTGGGAAATCTCAGGCTTGA 2300
2301 AGAGTGTCGAATTATGTCTTCTGCAGGCAAGGCCACTGTGGTTGAATTGGG 2350
|||||
2301 AGAGTGTCGAATTATGTCTTCTGCAGGCAAGGCCACTGTGGTTGAATTGGG 2350
2351 AGAACCAGACATCATGTCTCAGAGTTACTGTTCAGAAACAATGAGATCATC 2400
|||||
2351 AGAACCAGACATCATGTCTCAGAAATTACTCTTCAGAAACAATGAGATCATC 2400
2401 TTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTAT 2450
|||||
2401 TTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACCCCTTCAGATTAT 2450

FIG. 17K

2451 TCGTATTATGGAAATAATCTGGCAAAATCAAGGCTCTTGATCTTCGAATGT 2500
|||||
2451 TCGCATTATGGAAATAATCTGGCAAAATCAAGGCTCTTGATCTTCGAATGT 2500
|||||
2501 TACCTTATGGTTGTCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTG 2550
|||||
2501 TACCTTATGGATGTCTGTCAATCGGTGACTGTGTGGGACTTATCGAGGTG 2550
|||||
2551 GTGCGAAATTCTCACACTATTATGCAAAATTCAGTGCAAAAGCGGCTTGAA 2600
|||||
2551 GTGAGAAATTCTCACACTATAATGCAGATTTCAGTGTAAGGAGGCCTGAA 2600
|||||
2601 AGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGGCTCAAAGACA 2650
|||||
2601 AGGTGCACTGCAGTTTAACAGCCACACACTCCATCAGTGGCTCAAAGACA 2650
|||||
2651 AGAACAAAGGAGAAATATATGATGCAGCCATTGACCTGTTTACACGTTCA 2700
|||||
2651 AGAACAAAGGGGAAATATATGATGCGGCCATCGATTGTTTACACGATCA 2700
|||||

FIG. 17L

2701 TGTGCTGGATACTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCA 2750
|||||
2701 TGTGCTGGATAATTGTGTGCCACCTTCATTTTGGGAATTGGAGATCGTCA 2750

2751 CAATAGTAACATCATGCTGAAAGACGATGGACAACCTGTTTCATATAGATT 2800
|||||
2751 CAATAGTAATATCATGCTTAAAGATGATGGACAACCTGTTTCATATAGATT 2800

2801 TTGGACACTTTTGGATCACAAGAGAAAATTGGTTATAAACGAGAA 2850
|||||
2801 TTGGACACTTTTGGATCACAAGAGAAAATTGGTTATAAACGAGAG 2850

2851 CGTGTGCCAATTGTTTGGACACAGGATTTCTTAATAGTATTAGTAAAGG 2900
||
2851 CGCGTGCCGTTTGTGTTTGGACACAAGATTTCTTAATAGTATTAGTAAAGG 2900

2901 AGCCCAAGAATGCACAAGACAAGAGAAATTGAGAGGTTTCAGGAGATGT 2950
|||||
2901 AGCCCAAGAATGCACAAGACAAGAGAAATTGAGAGGTTTCAGGAGATGT 2950

FIG. 17M

2951 GTTACAAGGCTTATCTAGCTATTTCGACAGCATGCCAATCTTCATAAAT 3000
|||||
2951 GTTACAAGGCTTATCTAGCTATTTCGGCAGCATGCCAATCTTCATAAAT 3000
3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGA 3050
|||||
3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTGCAATCTTTTGA 3050
3051 TGACATTGCATACATTCCGAAAGACCCCTAGCCTTAGATAAACTGAGCAAG 3100
|||||
3051 TGATATTGCATACATTCCGAAAGACCCCTAGCCTTAGATAAACTGAGCAAG 3100
3101 AGGCTTTGGAGTATTTCATGAAACAATAATGAATGATGCACATCATGGTGGC 3150
|||||
3101 AGGCTTTGGAGTATTTCATGAAACAATAATGAATGATGCACACCATGGTGGC 3150
3151 TGGACAACAATAATGGATTGGATCTTCCACACAATAATAACAGCATGCATT 3200
|||||
3151 TGGACAACAATAATGGATTGGATCTTCCACACAATAATAAGCAGCATGCTTT 3200
3201 GAACTGAAAGATAAAGTGAAGAAATGAAAGCTCACTCTGGA
|||||
3201 GAACTGA.....

FIG. 18A

| | | | | | |
|-----|--|-----|-----|-----|-----|
| 10 | 20 | 30 | 40 | 50 | 60 |
| h | MPPRPSSGELWGIHLMPPRIILVECLLPNGMIVTLECLREATLVTIKHSELFKEARKYPLHQ | | | | |
| | | | | | |
| b | MPPRPSSGELWGIHLMPPRIILVECLLPNGMIVTLECLREATLVTIKHSELFKEARKYPLHQ | | | | |
| 10 | 20 | 30 | 40 | 50 | 60 |
| 70 | 80 | 90 | 100 | 110 | 120 |
| h | LLQDESSYIFVSVTQEAEREFFDETRRLCDLRLFPFLKVIEPVGNGNREEKILNREIGFA | | | | |
| | | | | | |
| b | LLQDESSYIFVSVTQEAEREFFDETRRLCDLRLFPFLKVIEPVGNGNREEKILNREIGFA | | | | |
| 70 | 80 | 90 | 100 | 110 | 120 |
| 130 | 140 | 150 | 160 | 170 | 180 |
| h | IGMPVCEFDMPVKDPEVQDFERRNILNVCKEAVDLRDLNSPHSRAMYVYPHVESSELPKH | | | | |
| | | | | | |
| b | IGMPVCEFDMPVKDPEVQDFERRNILNVCKEAVDLRDLNSPHSRAMYVYPHVESSELPKH | | | | |
| 130 | 140 | 150 | 160 | 170 | 180 |

| | | | | | | | | | | |
|---|--------------|---------------------------------------|---------------|----------|--------|--------|--------|--------|--------|--------|
| h | IYNKLDRGQII | VVIVSPNNDKQYTLKINHDCVPEQVIAEAI | RKKTRSM | LLSSEQLK | 190 | 200 | 210 | 220 | 230 | 240 |
| b | IIIIII: | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII |
| b | IYNKLDKGQII | VVIVSPNNDKQYTLKINHDCVPEQVIAEAI | RKKTRSM | LLSSEQLK | 190 | 200 | 210 | 220 | 230 | 240 |
| h | LCVLEYQGKYIL | KVCGCDEYFLEKYPLSQYKYIRSCIMLGRMPNLKMM | AKESLYSQLPMD | | 250 | 260 | 270 | 280 | 290 | 300 |
| b | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII |
| b | LCVLEYQGKYIL | KVCGCDEYFLEKYPLSQYKYIRSCIMLGRMPNLML | MAKESLYSQLPMD | | 250 | 260 | 270 | 280 | 290 | 300 |
| h | CFTMPYSRR | ISTATPYMNGETSTKSLWVINRALRIKILCATYVNLN | IRDIDKIYVRTGI | | 310 | 320 | 330 | 340 | 350 | 360 |
| b | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII | IIIIII |
| b | CFTMPYSRR | ISTATPYMNGETSTKSLWVINSALRIKILCATYVNVN | IRDIDKIYVRTGI | | 310 | 320 | 330 | 340 | 350 | 360 |

FIG. 18C

| | | | | | | |
|-----|----------------|--------|---------------|---------------|---------------------|-------------------|
| 370 | 380 | 390 | 400 | 410 | 420 | |
| h | YHGEPLCDNVNTQ | RVP | CSNPRW | NEWLNYDIYIPDL | PRAARLCL | SICSVKGRKGAKEEHC |
| | | | | | | |
| b | YHGEPLCDNVNTQ | RVP | CSNPRW | NEWLNYDIYIPDL | PRAARLCL | SICSVKGRKGAKEEHC |
| 370 | 380 | 390 | 400 | 410 | 420 | |
| 430 | 440 | 450 | 460 | 470 | 480 | |
| h | PLAWGNINLFDYTD | TLVSGK | MALNLWPVPHGLE | DLNPIGV | TG | SNPNKETPCLELEFDWF |
| | | | | | | |
| b | PLAWGNINLFDYTD | TLVSGK | MALNLWPVPHGLE | DLNPIGV | TG | SNPNKETPCLELEFDWF |
| 430 | 440 | 450 | 460 | 470 | 480 | |
| 490 | 500 | 510 | 520 | 530 | 540 | |
| h | SSVVKFPDMSVIEE | HANWSV | SREAGFSYSHAGL | SNRLARDN | ELRENDKEQLKAISTRDPL | |
| | | | | | | |
| b | SSVVKFPDMSVIEE | HANWSV | SREAGFSYSHAGL | SNRLARDN | ELRENDKEQLKAISTRDPL | |
| 490 | 500 | 510 | 520 | 530 | 540 | |

FIG. 18D

| | | | | | |
|-----|-----------------------------------|------------------------|---------------|----------|------|
| 550 | 560 | 570 | 580 | 590 | 600 |
| h | SEITEQEKDFLWSHRHYCVTPEILPKLLSVKWN | SRDEVAQMYCLVKDW | PP | IKPEQAME | |
| | | | | | |
| b | SEITEQEKDFLWSHRHYCVTPEILPKLLSVKWN | SRDEVAQMYCLVKDW | PP | IKPEQAME | |
| 550 | 560 | 570 | 580 | 590 | 600 |
| 610 | 620 | 630 | 640 | 650 | 660 |
| h | LLDCNYPDPMVRGFAVRCLEKYLTD | DKLSQYLIQLVQVLKYEQYLDN | LLVRFL | KKALTN | |
| | | | | | |
| b | LLDCNYPDPMVRGFAVRCLEKYLTD | DKLSQYLIQLVQVLKYEQYLDN | LLVRFL | KKALTN | |
| 610 | 620 | 630 | 640 | 650 | 660 |
| 670 | 680 | 690 | 700 | 710 | 720 |
| h | QRIGHFFFWHLKSEMHNKTVSQRFG | LLLESYCRACGM | YLKHLNRQVEAME | KLINLT | DILK |
| | | | | | |
| b | QRIGHFFFWHLKSEMHNKTVSQRFG | LLLESYCRACGM | YLKHLNRQVEAME | KLINLT | DILK |
| 670 | 680 | 690 | 700 | 710 | 720 |

FIG. 18E

| | | | | | | |
|---|--|-----------|--------------------|---------------------------|-----|-----|
| | 730 | 740 | 750 | 760 | 770 | 780 |
| h | QERKDETQKVQMKFLVEQMRPDMFMDALQGLLSP | LNPAHQ | LNRLKECRIMSSAKRPLW | | | |
| | | | | | | |
| | | | | | | |
| b | QEKDETQKVQMKFLVEQMRPDMFMDALQGLSPLN | PAHQ | LNRLKECRIMSSAKRPLW | | | |
| | 730 | 740 | 750 | 760 | 770 | 780 |
| h | LNWENPDIMSELLFQNN | EIFKNGDDL | RQDMLTLQ | IIRIMENIWQNQGLDLRMLPYGCLS | | |
| | 790 | 800 | 810 | 820 | 830 | 840 |
| | | | | | | |
| | | | | | | |
| b | LNWENPDIMSELLFQNN | EIFKNGDDL | RQDMLTLQ | IIRIMENIWQNQGLDLRMLPYGCLS | | |
| | 790 | 800 | 810 | 820 | 830 | 840 |
| h | IGDCVGLIEVVRNSHTIMQIQCKGGLKGALQFNSHTLHQWLKDKNKGEIYDAIDLFTS | | | | | |
| | 850 | 860 | 870 | 880 | 890 | 900 |
| | | | | | | |
| | | | | | | |
| b | IGDCVGLIEVVRNSHTIMQIQCKGGLKGALQFNSHTLHQWLKDKNKGEIYDAIDLFTS | | | | | |
| | 850 | 860 | 870 | 880 | 890 | 900 |

FIG. 18F

| | | | | | |
|------|---|------|------|------|------|
| 910 | 920 | 930 | 940 | 950 | 960 |
| h | CAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPFVLTQDF | | | | |
| | | | | | |
| b | CAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPFVLTQDF | | | | |
| 910 | 920 | 930 | 940 | 950 | 960 |
| 970 | 980 | 990 | 1000 | 1010 | 1020 |
| h | LIVISKAQECTKTREFFERFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPPELQSFDDIA | | | | |
| | | | | | |
| b | LIVISKAQECTKTREFFERFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPPELQSFDDIA | | | | |
| 970 | 980 | 990 | 1000 | 1010 | 1020 |
| 1030 | 1040 | 1050 | 1060 | 1070 | 1080 |
| h | YIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTIKQHALNXXKITEKMKAHSG | | | | |
| | | | | | |
| b | YIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTIKQHALNXX | | | | |
| 1030 | 1040 | 1050 | 1060 | | |

FIG. 19A

1 MPFRPSSGEL WGIHMPPRI LVECLLPNGM IVTLECLREA TLVTIKHELF
51 KEARKYPLHQ LLQDESSYIF VSVTQEAERE EFFDETRRLC DLRLFQPFLLK
101 VIEPVGNREE KILNREIGFA IGMPVCEEDM VKDPEVQDFR RNILNVCKEA
151 VDLRDINSPH SRAMYVPPH VESSPELPKH IYNKLDRGQI IVVIWVIVSP
201 NNDKQKYTLK INHDCVPEQV IAEAIRKKTR SMLLSSEQLK LCVLEYQGKY
251 ILKVCGCDEY FLEKYPLSQY KYIRSCIMLG RMPNLKMMAK ESLYSQLPMD
301 CETMPSYSRR ISTATPYMNG ETSTKSLWVI NRALRIKILC ATYVNLNIRD
351 IDKIYVRTGI YHGGEPLCDN VNTQRVPCSN PRWNEWLNVD IYIPDLPRAA
401 RLCLSICSVK GRKGAKKEHC PLAWGNINLF DYTDTLVSGK MALNLWVPVPH
451 GLEDLLNPIG VTGSNPKNKET PCLELEFDWF SSVVKFPDMS VIEEHANWSV

FIG. 19B

501 SREAGFSYSH AGLSNRLARD NELRENDKEQ LKAISTRDPL SEITEQEKDF
551 LWSHRHYCVT IPEILPKILL SVKWSRDEV AQMYCLVKDW PPIKPEQAME
601 LLDNCYPDPM VRGFAVRCLE KYLTDDKLSQ YLIQLVQVLK YEQYLDNLLV
651 RFLKKALTN QRIGHFFFWH LKSEMHNKTV SQRFGLLES YCRACGMYLK
701 HLNQVEAME KLINLTDILK QERKDETQKV QMKFLVEQMR RPDFMDALQG
751 LLSPLNPAHQ LGNLRLECR IMSSAKRPLW LNWENPDIMS ELLFQNNELI
801 FKNGDDLQRD MLTLQIIRIM ENIWQNQGLD LRMLPYGCLS IGDCVGLIEV
851 VRNSHTIMQI QCKGGLKGAL QFNSHTLHQW LKDKNKGEIY DAAIDLFTRS
901 CAGYCVATFI LGIGDRHNSN IMVKDDGQLF HIDFGHFLDH KKKKFGYKRE
951 RVPFVLTQDF LIVISKGAQE CTKTREFFERF QEMCYKAYLA IRQHANLFIN
1001 LFSMMLGSGM PELQSFDDIA YIRKTLALDK TEQEALEYFM KOMNDAHGG
1051 WTTKMDWIFH TIKQHALN*

FIG. 20

1 GGAGACGACTTGCACAGGATCAACTTATTCTTCAAATCATTTCACTC
GlyAspAspLeuArgGlnAspGlnLeuIleLeuGlnIleIleSerLeu

49 ATGGACAAGCTGTACGGAAAGAAATCTGGACTTGAAATTGACACCT
MetAspLysLeuLeuArgLysGluAsnLeuAspLeuLysLeuThrPro

97 TATAAGGTGTAGCCACGACAGTACAAACATGGCTTCATGCAGtTTATC
TyrLysValLeuAlaThrSerThrLysHisGlyPheMetGlnPheIle

145 CAGTCAGTtCCTGTGGCTGAaGTTCTTGATACAGAGGAAGCATTGAG
GlnSerValProValAlaGluValLeuAspThrGluGlySerIleGln

193 AACTTTTtagAAAATATGCACCAAGTGAGAAATGGCCAAATGGGATT
AsnPheArgLysTyrAlaProSerGluAsnGlyProAsnGlyIle

241 AGTGCTGAGGTCATGGACACTtACGTTAAAGCTGTGCTGGATATTGC
SerAlaGluValMetAspThrTyrValLysSerCysAlaGlyTyrCys

289 GTGATCACCTATATACTTGAGTTGGAGACAGGCACCTGGATAACCTT
ValIleThrTyrIleLeuGlyValGlyAspArgHisLeuAspAsnLeu

337 TTGCTAACCAAAACAGGCAAACTCTCCACATCGATTTCGGCCAC
LeuLeuThrLysThrGlyLysLeuPheHisIleAspPheGlyHis

FIG. 21

1 GGGGATGACTTACGGCAGGACATGCTAACGCTGCAGATGATTCGCATC
GlyAspLeuArgGlnAspMetLeuThrLeuGlnMetIleArgIle

49 ATGAGCAAGATCTGGGTCCAGGAGGGGCTGGACATGCCATGGTCATC
MetSerLysIleTrpValGlnGluGlyLeuAspMetArgMetValIle

97 TTCCGCTGCTTCTCCACCGCGCGGCGAGAGGATGGTGAGATGATC
PheArgCysPheSerThrGlyArgGlyArgGlyMetValGluMetIle

145 CCTAATGCTGAGACCCCTGCGTAAGATCCAGGTGGAGCATGGGGTGACC
ProAsnAlaGluThrLeuArgLysIleGlnValGluHisGlyValThr

193 GGCTCGTTCAAGGACCGGCCCTGGCAGACCGGCTGCAGAAACACAAC
GlySerPheLysAspArgProLeuAlaAspArgLeuGlnLysHisAsn

241 CCTGGGAGGACGAGTATGAGAAGGCTGTGGaGAACCTTATCTACTCC
ProGlyGluAspGluTyrGluLysAlaValGluAsnPheIleTyrSer

289 TGGCTGGCTGCTGCGTGGCCACGTACGTCTTGGGCATCTGTGACCga
CysAlaGlyCysCysValAlaThrTyrValLeuGlyIleCysAspArg

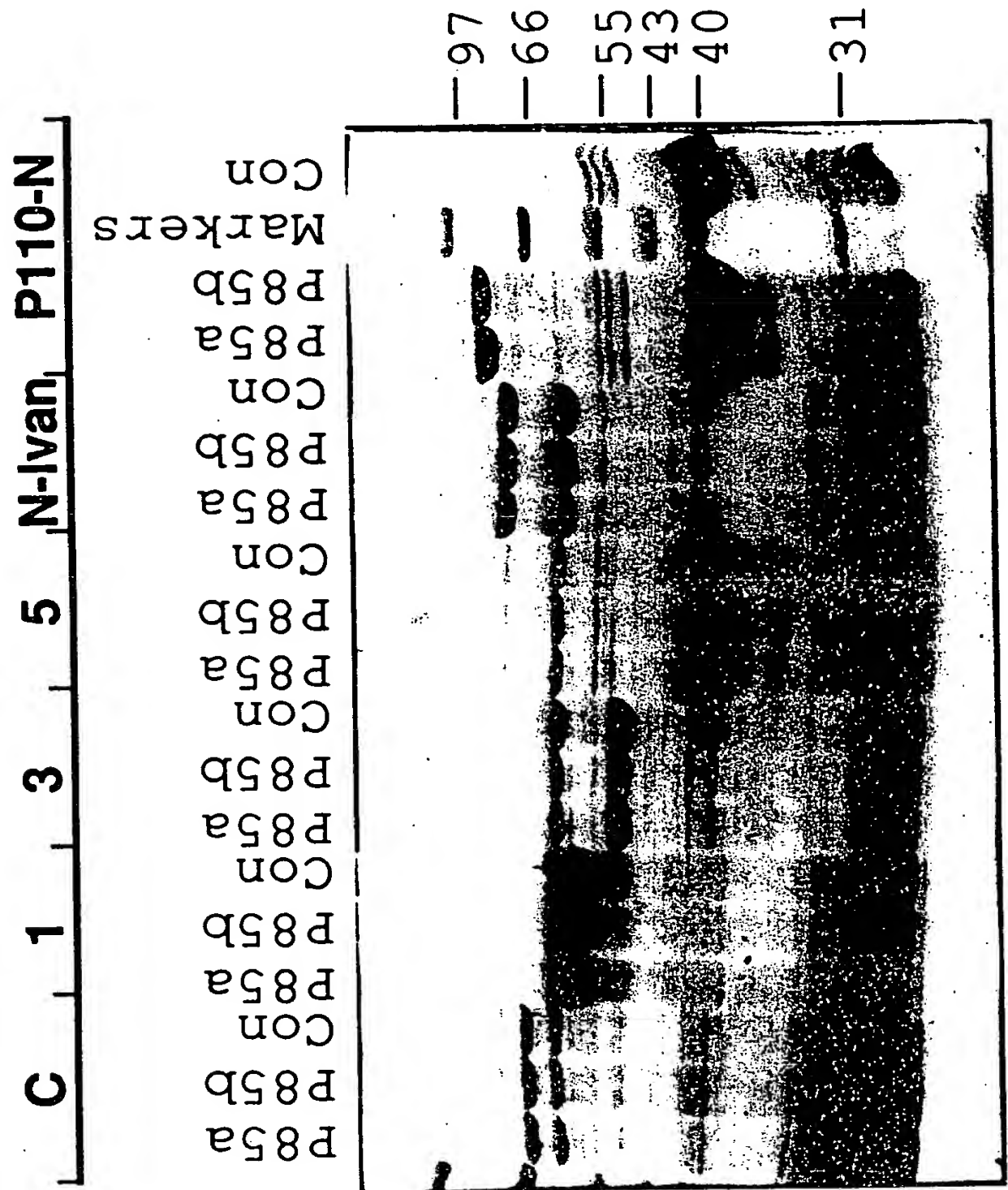
337 CATAATGACAACATCATGCTGAAGACCACCTGGTCACATGTTCCACATC
HisAsnAspAsnIleMetLeuLysThrThrGlyHisMetPheHisIle

385 GACTTCGGC
AspPheGly

FIG. 22

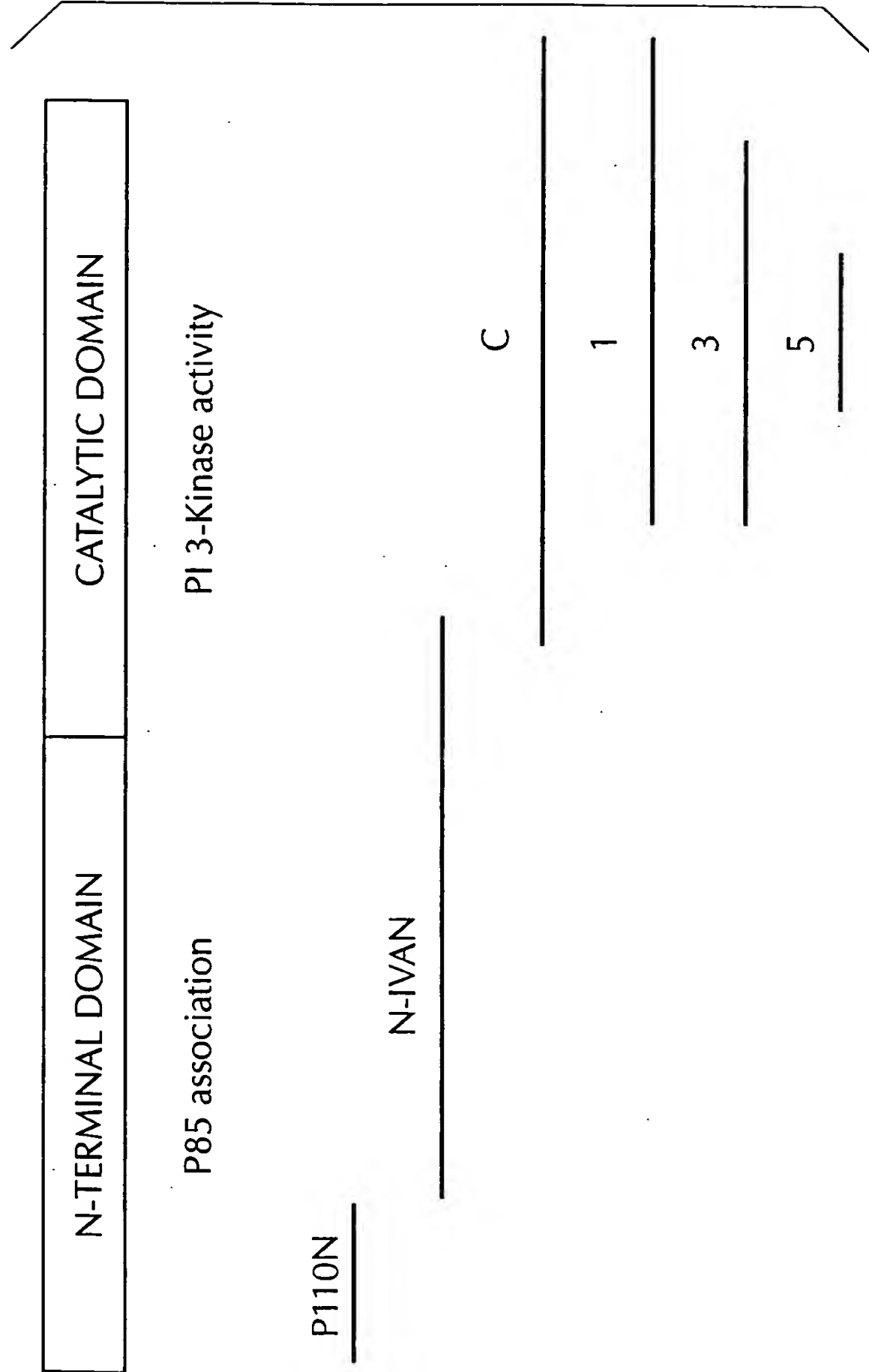
| | | |
|-----------|--|-----|
| 1 | GDDLQRQDqLvVQIIslMnellknEnvDLkLtPYkiLaTGpgeGaIEfipN | 50 |
| vps34 | GDDLQRQDqLiLQIIslmdkllrkEnLDLkLtPYkvLaTstkhGFmqfIqs | |
| PITR-c | GDDLQRQDmLtLQIIriMeniwqnqGLDLrMLPYgclsiGdcvGLIEvVrN | |
| hump110 | GDDLQRQDmLtLQmIriMskiwvqEgLDMrMviFrcFSTGrgrGMVEmIpN | |
| PITR-f | GDDLQRQD-L-LQII-M-----E-LDL---PY--L-TG---G-IE-I-N | |
| Consensus | | |
| 51 | dtlasilskyhGIIGy.....LklhypdenAtlqVqgwvLDnFVksCA | 100 |
| vps34 | vpvaevldtegsIqnf.....FrkYapseNgpngIsaevmDtYVksCA | |
| PITR-c | shtimqi qckgGlkGalqfnshLtLhqWlkdKNkge.IydaaiDLftrSCA | |
| hump110 | aetlrkiqvehGVtGs..fkdrpLadrLqkhNpgedeyekavEnFIySCA | |
| PITR-f | -----GI-G-----L-----N-----I-----D-FV-SCA | |
| Consensus | | |
| 101 | | 133 |
| vps34 | GYCViTYILGVGDRH1DN1LvtpdGhFFHaDFG | |
| PITR-c | GYCViTYILGVGDRH1DN1L1tkGkLFHIDFG | |
| hump110 | GYCVaTFILGIGDRHnsNiMvkddGqLFHIDFG | |
| PITR-f | GCCVaTYVLGicDRHnDNiMlktGhMFHIDFG | |
| Consensus | GYCV-TYILG-GDRH-DN-----G-LFHIDFG | |

FIG. 23A



+

FIG. 23B



+



FIG. 25A

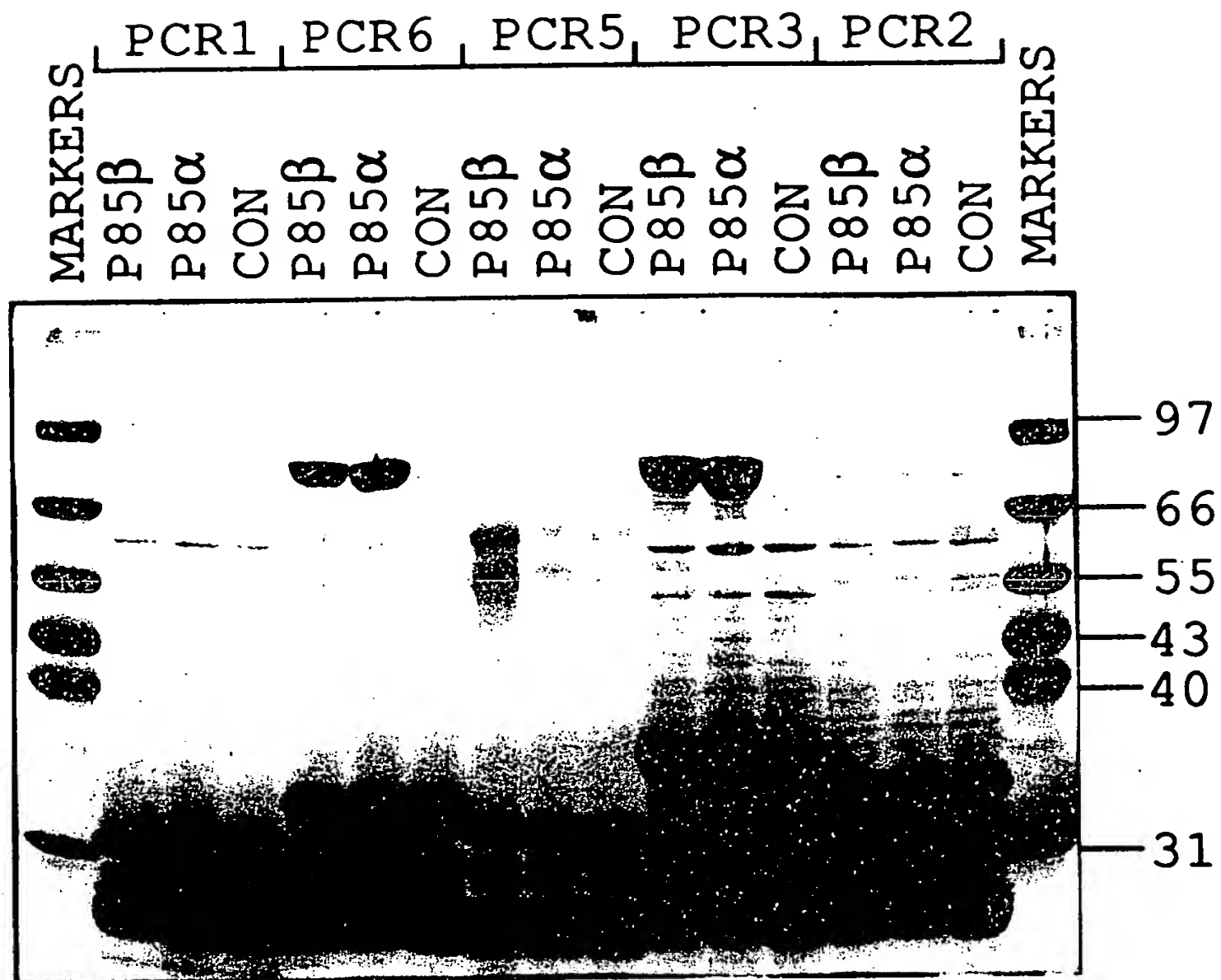


FIG. 25B

